

GenCore version 5.1.4-p5-A578
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OM protein - protein search, using sw model

Run on: March 21, 2003, 11:55:50 ; Search time 18.0323 Seconds

(without alignments)
317.751 Million cell updates/sec

Title: US-09-682-706-3

Perfect score: 200
Sequence: 1 HPGSRIVSLDVIIGLLQLL.....ARARAREQATTNARIARV 43

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*

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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	191	95.5	112	23	AAO15170 Human stresscopin
2	191	95.5	112	23	AAE21006 Human urocortin-re
3	161	80.5	38	23	AAE21009 Human urocortin-re
4	161	80.5	41	23	AAE21007 Human mature uroco
5	133	66.5	112	23	AAE21008 Mouse urocortin II
6	72	36.0	161	23	AAO15171 Human stresscopin
7	69	34.5	41	13	[Gln2, Glu29, Leu3
8	66	33.0	36	13	[Nle18, 21, Arg36]-
9	66	33.0	38	13	[des-AA1-3, Glu29,
10	66	33.0	39	13	[des-Ser1, des-Gln

11	66	33.0	40	6	AAp50922	Rat corticotliberin
12	66	33.0	41	13	AAE25782	[Val1, Ser2, Arg36
13	65	32.5	41	13	AAE25796	[Ala13]-Arg23-alpha
14	65	32.5	41	13	AAE25778	[Glu1, Leu33, Glu4
15	65	32.5	41	13	AAE25781	[Thr22, Glu29, 40,
16	65	32.5	41	13	AAE29094	[Ala39]-rCRF. Syn
17	65	32.5	41	16	AAE79047	Corticotropin rele
18	64	32.0	38	13	AAE25779	[des-Ser1-Glu2-Glu
19	64	32.0	41	13	AAE25797	[Leu12, Glu13, Tyr
20	64	32.0	41	13	AAE25798	[CM10,14,19,27,33
21	64	32.0	41	13	AAE25780	[Nle21,38, Glu29,
22	64	32.0	41	13	AAE32488	[Ala39]-AHC. Syn
23	64	32.0	42	6	AAp50920	Rat corticotliberin
24	63	31.5	39	18	AAE22395	Human urocortin pe
25	63	31.5	40	18	AAW37078	Rat urocortin pept
26	63	31.5	40	18	AAW22393	Rat urocortin. Ra
27	63	31.5	40	22	AAU09088	Corticotropin-rele
28	63	31.5	40	22	AAE90923	Corticotropin rele
29	63	31.5	40	22	AAE90924	Corticotropin rele
30	63	31.5	40	22	AAE67697	Amino acid sequenc
31	63	31.5	40	22	AAE67698	Mouse monoclonal a
32	63	31.5	40	23	AAO14289	[CM10,15,27,37, C
33	63	31.5	41	13	AAE25799	Arg23-alpha helica
34	63	31.5	41	13	AAE25777	[Nle18, 21, Arg23, 2
35	63	31.5	41	13	AAE25805	Corticotropin rele
36	63	31.5	41	22	AAE90921	Corticotropin rele
37	63	31.5	41	22	AAE90922	Rat corticotliberin
38	63	31.5	44	6	AAp50921	Human precursor ur
39	63	31.5	124	18	AAW22392	Human urocortin.
40	63	31.5	124	21	AAE49943	Corticotropin rele
41	62	31.0	41	11	AAE02205	Mouse monoclonal a
42	62	31.0	41	23	AAO14290	Mammalian VIP faml
43	62	30.5	41	23	ABO06666	Rat and sheep cort
44	61	30.5	38	6	AAp50914	[Id-Pro, Nle21,38,
45	61	30.5	38	13	AAE25811	

ALIGNMENTS

RESULT 1	AAO15170	standard; Protein: 112 AA.
ID	AAO15170	
AC	AAO15170:	
XX	02-SEP-2002	(first entry)
DE	Human stresscopin 1 protein.	
XX	Human: stresscopin 1; weight reduction; gene therapy;	
KW	corticotropin releasing hormone receptor 2 activator;	
KW	appetite suppression; cardioprotection; inflammation; heart disease;	
KW	organ graft rejection; hypertension; trauma stress; dysrhythmia; oedema;	
KW	skin disease; inflammatory arthritis; rheumatoid arthritis;	
KW	non-infectious inflammatory arthropathy; stress-related disorder.	
OS	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
FT	Peptide	1..66
FT	Protein	/label= Signal_peptide
FT		67..112
FT	Misc-difference	/note="Mature stresscopin 1 protein"
FT		/note="This region is illegible in the specification and has been generated by decoding the corresponding nucleotide (AA143490)"
XX	WO200234934-A2.	
XX		
XX	02-MAY-2002.	
XX		

PF 10-OCT-2001; 2001WO-US32065.
XX
XX 26-OCT-2000; 2000US-244128P.
PR 15-MAR-2001; 2001US-276615P.
XX
XX (STRD) UNIV LELAND STANFORD JUNIOR.
PA
XX
XX Hsu SY, Heueh AJW;
PI
XX
XX WPI: 2002-471444/50.
DR N-PSDB: AAL43490.
XX
XX
XX Composition comprising human stresscopin 1 or stresscopin 2
PT polypeptide, useful in appetite suppression, for cardioprotection,
PT reducing edema, reducing inflammation, organ graft rejection, reducing
PI hypertension
XX
XX
XX Claim 2; Fig 1A; 50pp; English.
PS
XX
XX The invention comprises the amino acid and coding sequences of two human
CC proteins which activate the corticotropin releasing hormone receptor 2
CC (CRH-R2). The proteins of the invention are called stresscopin 1 and
CC stresscopin 2. The stresscopin DNA and protein sequences of the invention
CC are useful for appetite suppression, cardioprotection, reducing edema,
CC reducing inflammation, reducing organ graft rejection, reducing
CC hypertension and reducing trauma stress. The stresscopin DNA and protein
CC sequences are also useful for the treatment of dysthymia, skin diseases,
CC inflammatory arthritis, non-infectious inflammatory arthropathy (e.g.
CC rheumatoid arthritis), heart disease and stress-related disorders. The
CC present amino acid sequence represents the human stresscopin 1 protein.
XX
XX
XX Sequence 112 AA;
SQ
Query Match 95.5%; Score 191; DB 23; Length 112;
Best Local Similarity 95.3%; Pred. No. 1.2e-19;
Matches 41; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 HPGSRIVSLDVIIGLQILLEQARARAREQATTNARILAV 43
DB 67 HPGSRIVSLDVIIGLQILLEQARARAREQATTNARILAV 109
|||||
RESULT 2
AAE21006
ID AAE21006 standard; Protein; 112 AA.
XX
XX AAE21006;
AC
XX
XX 01-JUL-2002 (first entry)
DT
XX
XX Human urocortin-related peptide (URP) protein.
DE
XX
XX Human; urocortin-related peptide; URP; antipyretic; cardiact; urocortin;
KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
XX stress; anxiety.
OS
XX Homo sapiens.
FH
XX Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 72..112
FT /label= Mature_URP_protein
FT Modified-site 112
FT /note= "C-terminal amide"
XX
XX WO200212307-A1.
XX
XX 14-FEB-2002.
PD
XX
XX 31-JUL-2001; 2001WO-US23976.
PF
XX
XX 04-AUG-2000; 2000US-223255P.
PR

PR 07-MAR-2001; 2001US-273969P.
XX
XX (RERE-) RES DEV FOUND.
PA
XX
XX Vale WM, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
PI Hogenesch JB, Perrin MH.
XX
XX
XX WPI: 2002-241737/29.
DR N-PSDB: AAD33401.
XX
XX
XX Novel urocortin II polypeptide or human urocortin-related peptide, for
PT treating high body temperature, appetite dysfunction, congestive heart
PT failure, stress, anxiety and low levels of adrenocortico tropic hormone
XX
XX
XX Claim 18; Fig 1; 94pp; English.
PS
XX
XX The invention relates to a modified protein selected from urocortin II
CC (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
CC composition is useful for treating a pathophysiological state including
CC high body temperature, appetite dysfunction, congestive heart failure,
CC stress, anxiety and undesirably low levels of adrenocortico tropic
CC hormone (ACTH) secretions. A modified protein conjugate is useful in
CC scintigraphy and in various assays, and also for the targeted
CC destruction of corticotropin-releasing factor (CRF) receptor bearing
CC cells. The present sequence is human URP protein.
XX
XX
XX Sequence 112 AA;
SQ
Query Match 95.5%; Score 191; DB 23; Length 112;
Best Local Similarity 95.3%; Pred. No. 1.2e-19;
Matches 41; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 HPGSRIVSLDVIIGLQILLEQARARAREQATTNARILAV 43
DB 67 HPGSRIVSLDVIIGLQILLEQARARAREQATTNARILAV 109
|||||
RESULT 3
AAE21009
ID AAE21009 standard; peptide; 38 AA.
XX
XX AAE21009;
AC
XX
XX 01-JUL-2002 (first entry)
DT
XX
XX Human urocortin-related peptide (URP).
DE
XX
XX Human; urocortin-related peptide; URP; antipyretic; cardiact; urocortin;
KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
XX stress; anxiety.
OS
XX Homo sapiens.
FH
XX Key Location/Qualifiers
FT Modified-site 38
FT /note= "C-terminal amide"
XX
XX WO200212307-A1.
XX
XX 14-FEB-2002.
PD
XX
XX 31-JUL-2001; 2001WO-US23976.
PF
XX
XX 04-AUG-2000; 2000US-223255P.
PR 07-MAR-2001; 2001US-273969P.
XX
XX (RERE-) RES DEV FOUND.
PA
XX
XX Vale WM, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
PI Hogenesch JB, Perrin MH.
XX
XX
XX WPI: 2002-241737/29.
DR

XX

Query Match	Score	DB	Length
66.5%;	133;	23;	112;

Db 6 ISLDTFHLREVLQEMARAEQALAEQAHNSNRLL 38

RESULT 8

AAR25810

ID AAR25810 standard; peptide; 36 AA.

XX AAR25810;

DT 21-JAN-1993 (first entry)

DE [Nle18, 21, Arg36]-AAHC(6-41).

KW Corticotropin-releasing factor; cytotoxin; ACTH; AAHC; beta-endorphin; beta-lipotropin; pro-opiomelanocortin; corticosterone; gelonin; rat Amunine; alpha-helix; Arg23-alpha-helical CRF.

XX Synthetic.

OS Key Location/Qualifiers

FH Modified-site 13 /label= Nle

FT Modified-site 16 /label= Nle

FT Modified-site 36 /note= "amidated"

FT /note= "amidated"

PN US5132111-A.

XX 21-JUL-1992.

PF 22-JUN-1987; 87US-0065273.

PR 22-JUN-1987; 87US-0065273.

PR 11-APR-1990; 90US-0508258.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

PI Rivier JEF, Schwartz J, Vale WM;

DR WPI; 1992-267898/32.

CRF analogue and cytotoxic protein conjugates regulate ACTH secretion - for treating neoplasia associated with CRF expressing tumours and hyperactivity of the hypothalamus-pituitary adrenal axis

XX Example 39; Column 24; 16pp; English.

XX This peptide is disclosed as an analogue of CRF which lacks side-chain amino groups and has substitutions which give the peptide high alpha-helical forming potential. The peptide is a deriv. of a peptide designated Arg23-alpha-helical CRF or AAHC 1 to 5 residues. However, if shortened to eliminate residues 1-7, 1-8 or 1-9, competitive antagonists of CRF are formed. The peptide is used in a conjugate with cytotoxic protein. The peptide is joined to the cytotoxin via a dialdehyde linker attached via the alpha-amino group of the amino acid residue at position 1 of the analogue. The conjugates have high affinity for CRF receptors without exhibiting undesirable polymerisation and/or cross-linking anomalies. When the peptide was conjugated to gelonin using glutaraldehyde it was shown to be biologically active to selectively eliminate CRF target cells. The peptide also stimulates the secretion of ACTH and beta-endorphin.

SQ Sequence 36 AA;

Query Match 33.0%; Score 166; DB 13; Length 36;
Best Local Similarity 48.5%; Pred. No. 0.027; 13; Indels 0; Gaps 0;
Matches 16; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 8 LSLDVLIGLILQLLEQARARAREQATTNARIL 40

Db 1 ISLDTFHLREVLQEMARAEQALAEQAHNSNRLL 33

RESULT 9

AAR25787

ID AAR25787 standard; peptide; 38 AA.

XX AAR25787;

DT 21-JAN-1993 (first entry)

DE [des-AA1-3, Glu29, 40, Arg36, Tyr37]-rCRF(4-41).
XX rat: corticotropin-releasing factor; cytotoxin; ACTH; beta-endorphin; beta-lipotropin; pro-opiomelanocortin; corticosterone; gelonin; rat Amunine.

XX Rattus rattus.

OS Key Location/Qualifiers

FH Modified-site 38 /note= "amidated"

FT Modified-site 38 /note= "amidated"

FT /note= "amidated"

PN US5132111-A.

XX 21-JUL-1992.

PF 22-JUN-1987; 87US-0065273.

PR 22-JUN-1987; 87US-0065273.

PR 11-APR-1990; 90US-0508258.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

PI Rivier JEF, Schwartz J, Vale WM;

DR WPI; 1992-267898/32.

CRF analogue and cytotoxic protein conjugates regulate ACTH secretion - for treating neoplasia associated with CRF expressing tumours and hyperactivity of the hypothalamus-pituitary adrenal axis

XX Example 16; Column 18; 16pp; English.

XX This peptide is disclosed as an analogue of rat CRF which lacks side-chain amino groups. It is used in a conjugate with cytotoxic protein (e.g. gelonin). The peptide is joined to the cytotoxin via a dialdehyde linker attached via the alpha-amino group of the amino acid residue at position 1 of the analogue. The conjugates have high affinity for CRF receptors without exhibiting undesirable polymerisation and/or cross-linking anomalies. When the peptide was conjugated to gelonin using glutaraldehyde it was shown to be biologically active to selectively eliminate CRF target cells. The peptide also stimulates the secretion of ACTH and beta-endorphin.

SQ Sequence 38 AA;

Query Match 33.0%; Score 66; DB 13; Length 38;
Best Local Similarity 41.7%; Pred. No. 0.029;
Matches 15; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 8 LSLDVLIGLILQLLEQARARAREQATTNARIL 43

Db 3 ISLDTFHLREVLQEMARAEQALAEQAHNSNRMEEI 38

RESULT 10

AAR25786

ID AAR25786 standard; peptide; 39 AA.

XX

PR 11-APR-1990; 90US-0508258.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

PI Rivier JEF, Schwartz J, Vale WM;

DR WPI; 1992-267898/32.

PT CRF analogue and cytotoxic protein conjugates regulate ACTH
secretion - for treating neoplasia associated with CRF expressing
tumours and hyperactivity of the hypothalamus-pituitary adrenal
axis

PS Example 11; Column 17; 16pp; English.

CC This peptide is disclosed as an analogue of rat CRF which lacks
side-chain amino groups. It is used in a conjugate with cytotoxic
protein (e.g. gelonin). The peptide is joined to the cytotoxin via
a di-aldehyde linker attached via the alpha-amino group of the amino
acid residue at position 1 of the analogue. The conjugates have
CC high affinity for CRF receptors without exhibiting undesirable
CC polymerisation and/or cross-linking anomalies. When the peptide was
CC conjugated to ricin A chain using glutaraldehyde it was shown to be
biologically active to selectively eliminate CRF target cells. The
CC peptide also stimulates the secretion of ACTH and beta-endorphin.

XX Sequence 41 AA;

SO Query Match 33.0%; Score 66; DB 13; Length 41;

Best Local Similarity 38.9%; Pred. No. 0.031; Matches 14; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

OY 8 LSLDVTLLGLLQTLLEQARARARAEQATTNARILAV 43

DB 6 ISLDTFLHLREVLMAAREQALQAHSNRRLMEET 41

RESULT 13

ID AAR25796 standard; peptide; 41 AA.

AC AAR25796;

DT 21-JAN-1993 (first entry)

DE [Ala13]-Arg23-alpha-helical CRF.

KW Corticotropin-releasing factor; cytotoxin; ACTH; AAHC;

KW beta-endorphin; beta-lipotropin; pro-opiomelanocortin;

KW corticosterone; gelonin; rat Amunine; alpha-helix.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 41

PN /note= "amidated"

XX US5132111-A.

PD 21-JUL-1992.

PE 22-JUN-1987; 87US-0065273.

XX 22-JUN-1987; 87US-0065273.

PR 11-APR-1990; 90US-0508258.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

PI Rivier JEF, Schwartz J, Vale WM;

DR WPI; 1992-267898/32.

XX CRF analogue and cytotoxic protein conjugates regulate ACTH

PT secretion - for treating neoplasia associated with CRF expressing

PT tumours and hyperactivity of the hypothalamus-pituitary adrenal
axis

PS Example 22; Column 20; 16pp; English.

CC This peptide is disclosed as an analogue of CRF which lacks
side-chain amino groups and has substitutions which give the
CC peptide high alpha-helical forming potential. The peptide is a
CC deriv. of a peptide designated Arg23-alpha-helical CRF or AAHC
CC which remains potent even if shortened at the N-terminus by from
CC 1 to 5 residues. However, if shortened to eliminate residues 1-7,
CC 1-8 or 1-9, competitive antagonists of CRF are formed. The peptide
CC is used in a conjugate with cytotoxic protein. The peptide is joined
CC to the cytotoxin via a di-aldehyde linker attached via the alpha-amino
CC group of the amino acid residue at position 1 of the analogue. The
CC conjugates have high affinity for CRF receptors without exhibiting
CC undesirable polymerisation and/or cross-linking anomalies. When the
CC peptide was conjugated to ricin A chain using glutaraldehyde it was
CC shown to be biologically active to selectively eliminate CRF target
CC cells. The peptide also stimulates the secretion of ACTH and
beta-endorphin.

XX Sequence 41 AA;

SO Query Match 32.5%; Score 65; DB 13; Length 41;

Best Local Similarity 45.5%; Pred. No. 0.043; Matches 15; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

OY 8 LSLDVTLLGLLQTLLEQARARARAEQATTNARIL 40

DB 6 ISLDTFLHLREVLMAAREQALQAHSNRRLMEET 38

RESULT 14

ID AAR25778 standard; peptide; 41 AA.

AC AAR25778;

DT 21-JAN-1993 (first entry)

DE [Gly1, Leu33, Glu40]-rCRF.

KW rat; corticotropin-releasing factor; cytotoxin; ACTH;

KW beta-endorphin; beta-lipotropin; pro-opiomelanocortin;

KW corticosterone; gelonin; rat Amunine.

OS Rattus rattus.

XX Key Location/Qualifiers

FT Modified-site 41

PN /note= "amidated"

XX US5132111-A.

PD 21-JUL-1992.

PE 22-JUN-1987; 87US-0065273.

XX 22-JUN-1987; 87US-0065273.

PR 11-APR-1990; 90US-0508258.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

PI Rivier JEF, Schwartz J, Vale WM;

DR WPI; 1992-267898/32.

XX CRF analogue and cytotoxic protein conjugates regulate ACTH

PT secretion - for treating neoplasia associated with CRF expressing

PT tumours and hyperactivity of the hypothalamus-pituitary adrenal

axis

XX Example 7; Column 16; 16pp; English.
 PS
 CC This peptide is disclosed as an analogue of rat CRF which lacks
 CC side-chain amino groups. It is used in a conjugate with cytotoxic
 CC protein (e.g. gelonin). The peptide is joined to the cytotoxin via
 CC a dialdehyde linker attached via the alpha-amino group of the amino
 CC acid residue at position 1 of the analogue. The conjugates have
 CC high affinity for CRF receptors without exhibiting undesirable
 CC polymerisation and/or cross-linking anomalies. When the peptide was
 CC conjugated to ricin A chain using glutaraldehyde it was shown to be
 CC biologically active to selectively eliminate CRF target cells. The
 CC peptide also stimulates the secretion of ACTH and beta-endorphin.
 XX
 SQ Sequence 41 AA;
 Query Match 32.5%; Score 65; DB 13; Length 41;
 Best Local Similarity 36.6%; Pred. No. 0.043;
 Matches 15; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
 OY 3 GSRVLSLVYILGLQILIEQARARARQATTNARILARY 43
 DB 1 GEEPPISLDLTFHLREVLREMARQALQQAHLNRRLMEI 41
 RESULT 15
 LD AAR25781 standard; peptide; 41 AA.
 AC AAR25781;
 XX
 DT 21-JAN-1993 (first entry)
 XX
 DE [Thr22, Glu29,40, Arg36]-rCRF.
 XX
 KW rat; corticotropin-releasing factor; cytotoxin; ACTH;
 KW beta-endorphin; beta-lipotropin; pro-opiomelanocortin;
 KW corticosterone; gelonin; rat Amunine.
 XX
 OS Rattus rattus.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 41
 FT /note="amided"
 XX
 PN US5132111-A.
 XX
 PD 21-JUL-1992.
 XX
 PF 22-JUN-1987; 87US-0065273.
 XX
 PR 22-JUN-1987; 87US-0065273.
 PR 11-APR-1990; 90US-0508258.
 XX
 (SALK) SALK INST BIOLOGICAL STUDIES.
 PI Rivier JEF, Schwartz J, Vale WW;
 XX
 DR WPI; 1992-267898/32.
 XX
 PT CRF analogue and cytotoxic protein conjugates regulate ACTH
 PT secretion - for treating neoplasia associated with CRF expressing
 PT tumours and hyperactivity of the hypothalamus-pituitary adrenal
 PT axis
 XX
 PS Example 10; Column 17; 16pp; English.
 CC This peptide is disclosed as an analogue of rat CRF which lacks
 CC side-chain amino groups. It is used in a conjugate with cytotoxic
 CC protein (e.g. gelonin). The peptide is joined to the cytotoxin via
 CC a dialdehyde linker attached via the alpha-amino group of the amino
 CC acid residue at position 1 of the analogue. The conjugates have
 CC high affinity for CRF receptors without exhibiting undesirable

CC polymerisation and/or cross-linking anomalies. When the peptide was
 CC conjugated to gelonin using glutaraldehyde it was shown to be
 CC biologically active to selectively eliminate CRF target cells. The
 CC peptide also stimulates the secretion of ACTH and beta-endorphin.
 XX
 SQ Sequence 41 AA;
 Query Match 32.5%; Score 65; DB 13; Length 41;
 Best Local Similarity 38.9%; Pred. No. 0.043;
 Matches 14; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
 OY 8 LSLDVYILGLQILIEQARARARQATTNARILARY 43
 DB 6 ISLDLTFHLREVLREMARQALQQAHLNRRLMEI 41

Search completed: March 21, 2003, 11:57:42
 Job time : 19.0323 secs

XX 01-NOV-2001.
 PD 20-APR-2001; 2001WO-US12865.
 XX 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX (CORI-) CORIXA CORP.
 XX Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 DR WPI: 2001-616774/71.
 DR N-PSDB: AAS39555.
 XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 PS Example 1; SEQ ID No 13684; 1069pp; English.
 XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 543 AA;
 SQ
 Query Match 14.0%; Score 80.5; DB 22; Length 543;
 Best Local Similarity 42.9%; Pred. No. 9.8;
 Matches 21; Conservative 5; Mismatches 20; Indels 3; Gaps 2;
 QY 21 PVTPTPTFQLRPQNSPQTTPPAASESPSAAPTW-MAQSHCSGTRHP 68
 DB 485 PVTSPPTTKRPPAAR--TPPTGTRKSPASGCPAYAPVHTPSPTPPP 531
 AAB33255
 ID AAB33255 standard; Protein: 192 AA.
 XX AAB33255;
 AC
 XX 25-JAN-2001 (first entry)
 DT
 XX Eucalyptus grandis transcription factor protein sequence #412.
 DE
 XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
 XX poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
 KW basic helix-loop-helix zipper; LIM domain; AP2; ERBS; zinc finger domain;
 KW homeodomain zipper; LIM domain; AP2; ERBS; zinc finger domain;
 KW type 2 Cys2His2; CCAAT box element; MYB.
 XX
 OS Eucalyptus grandis.
 XX

PN WO200053724-A2.
 XX 14-SEP-2000.
 PD 09-MAR-2000; 2000WO-US06112.
 XX 11-MAR-1999; 99US-0266513.
 PR 18-AUG-1999; 99US-0149485.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 PI Wood M, McGrath A, Shenk MA, Glenn M;
 XX WPI: 2000-579369/54.
 DR
 XX New isolated polynucleotide encoding a plant transcription factor for
 PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
 PT having modified gene expression or modified activity of a polypeptide
 PT -
 PS Claim 8; Page 696; 747pp; English.
 XX The present invention relates to novel plant transcription factors from
 CC Eucalyptus grandis or Pinus radiata. The present sequence is one such
 CC transcription factor. The transcription factor may be used to produce a
 CC plant having modified gene expression such as a woody plant e.g. a
 CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or
 CC factors of the present invention are members from the following families
 CC of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic
 CC helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain
 CC zipper, LIM domain, AP2 and ERBS, zinc finger domains of type 2
 CC Cys2His2, CCAAT box elements and MYB.
 CC
 XX Sequence 192 AA;
 SQ
 Query Match 13.9%; Score 80; DB 21; Length 192;
 Best Local Similarity 34.1%; Pred. No. 3.4;
 Matches 28; Conservative 12; Mismatches 32; Indels 10; Gaps 5;
 QY 16 RVLVVPVPIPTFQLRPQNSPQTTPR--PAASESPSA-PTWMAQSHCSGTRHP 71
 DB 115 KLLKMGIDPVTH---EPINKPKPTSEHPASLSSSQADPTSESPATH-QPNNAHDE 170
 QY 72 IVLSIDVPITGLL-QILLEGAR 91
 DB 171 VQLVVLPLVGLVRLLELLRGR 192
 Search completed: March 21, 2003, 11:57:41
 Job time : 47.9677 secs

W0200181581-A2

Page

of the human or animal body by therapy; and (3) an agent for creating

sq	sequence	1/14 aa,	14 0%:	Score 81:	DB 22:	length 774
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Query matchn

CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC XX

SO Sequence 111 AA;

Query Match 16.2%; Score 93.5; DB 22; Length 111;
 Best Local Similarity 29.3%; Pred. No. 0.085;
 Matches 27; Conservative 14; Mismatches 40; Indels 11; Gaps 2;

QY 7 LLWLMGRLVLP---VTPTPTQLRPNQSPQTPRPA-----SESSPAAPMP 55
 Db 15 LPLWPLTALLLLLPPLVTPPLPPAPADPAPAPAPAPAPAPAPAPAPAPAPPP 74
 QY 56 WAAQSHCSPTRRHPSRIVLSIDVPIGLQIIL 87
 Db 75 APPPADAPPAPEVEDNVLAVGVANGLVRL 106

RESULT 8
 AAY84593
 ID AAY84593 standard; Protein: 532 AA.
 XX

AC AAY84593;
 XX
 D7 25-JUL-2000 (first entry)
 XX

DE Amino acid sequence of a human artemin polypeptide.

XX Human; artemin; growth factor; neurotrophic factor; trophic support;
 KW neuron; trigeminal ganglion neuron; nodose ganglion neuron;
 KW superior cervical ganglion neuron; midbrain neuron; Alzheimer's disease;
 KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;
 KW Parkinson's disease; Huntington's disease; acute brain injury;
 KW acute spinal cord injury; nervous system tumour; blastoma;
 KW multiple sclerosis; infection; enteric disease; idiopathic constipation;
 KW Parkinson's disease; small cell lung carcinoma.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 536

FT /note= "encoded by CC"
 XX

GN WO200018799-A1.

XX 06-APR-2000.

PD 29-SEP-1999; 99WO-US22604.
 XX

PE 29-SEP-1998; 98US-0163283.
 XX

PR 12-NOV-1998; 98US-0108148.
 XX

PR 22-DEC-1998; 98US-0218698.
 XX

PA (UNIW) UNIV WASHINGTON.
 XX

PI Milbrandt JD, Baloh RH;
 XX

DR WPI: 2000-293109/25.
 XX

DR N-PSDB; AAI12548.
 XX

XX Isolated artemin growth factor proteins and the nucleic acids that
 PT encode them, useful for treating a range of degenerative neuronal
 PT disorders such as Parkinson's disease and Huntington's disease -
 CC

PS Disclosure: Fig 1A-C; 96pp; English.

XX The present sequence represents a human artemin growth factor protein.
 CC Artemin is a neurotrophic factor that belongs to the GDNF (glial cell
 CC line-derived neurotrophic factor)/neurturin/persephin family of growth
 CC factors and promotes differentiation, maintains mature phenotype and
 CC provides trophic support, promoting growth and survival of neurons.
 CC Artemin promotes the survival of trigeminal ganglion neurons, nodose

CC ganglion neurons, superior cervical ganglion neurons and tyrosine-
 CC hydroxylase-expressing dopaminergic ventral midbrain neurons. Artemin
 CC is the only member of the GDNF family that binds to GFR-alpha (growth
 CC factor receptor-alpha) and activates the GFR-alpha3/RET (Ret protein-
 CC tyrosine kinase) receptor complex and additionally, like GDNF and
 CC neurturin, artemin also binds to and activates GFRalpha1/RET. Artemin
 CC polypeptides and polynucleotides are administered to treat peripheral
 CC neuropathy, amyotrophic lateral sclerosis, Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease, ischemic stroke, acute brain
 CC injury, acute spinal cord injury, a nervous system tumour (e.g.
 CC blastoma), multiple sclerosis, infection or enteric disease (e.g.
 CC idiopathic constipation or constipation associated with Parkinson's
 CC disease, spinal cord injury or use of opiate pain killers). They may
 CC also be used to treat a patient suffering from small cell lung carcinoma.
 SO Sequence 532 AA;

Query Match 15.3%; Score 88.5; DB 21; Length 532;
 Best Local Similarity 30.9%; Pred. No. 1.6;
 Matches 25; Conservative 10; Mismatches 23; Indels 23; Gaps 4;

QY 11 VLMLGRLVLPVPTP-----IPTFQL-----RPNQSPQTPRPAASESPSA 51
 Db 160 LLWGLALRFLPMARSGSKPILPPPLSPSTOLGAHARBDLSPTAPAPGSSPSPPGC 219
 QY 52 PTWP---WAAQSHCSPTRRHPG 69
 Db 220 PLSPGSTWLSLRAC-PVAHFG 239

RESULT 9
 AAW22392
 ID AAW22392 standard; Protein: 124 AA.
 XX

AC AAW22392;
 XX

DT 07-OCT-1997 (first entry)
 XX

DE Human precursor urocortin.
 XX

KW Human; precursor; urocortin; corticotropin releasing factor; receptor;
 KW adrenocorticotrophic hormone; ACTH; affinity; rat; ovine; carp; urotensin;
 KW placenta; probe.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Protein 83..122

FT /note= "mature urocortin"
 XX

PN WO9700063-A2.

XX 03-JAN-1997.

PD 12-JUN-1996; 96WO-US10240.
 XX

PE 11-AUG-1995; 95US-0002223.
 XX

PR 13-JUN-1995; 95US-0490314.
 XX

PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX

PI Donaldson CJ, Lewis KA, Perrin MH, Rivier JEF, Sawchenko P;
 PI Vale WW, Vaughan J;
 XX

DR WPI: 1997-077344/07.
 XX

DR N-PSDB; AAT73432.
 XX

XX Urocortin peptide(s) related to urotensin and
 PT corticotropin-releasing factor - for increasing ACTH and
 PT beta-endorphin levels, lowering blood pressure and improving mood,
 PT memory and learning performance
 XX Claim 4; Page 82; 91pp; English.

Claim 2; Fig 1B; 50pp; English.

CC sequences (ABL01040
CC (ABR57737-ABB72072).

PI Vale MW, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
 PI Hogenesch JB, Perrin MH;
 DR WPI: 2002-241737/29.

XX Novel urocortin II polypeptide or human urocortin-related peptide, for
 PT treating high body temperature, appetite dysfunction, congestive heart
 PT failure, stress, anxiety and low levels of adrenocortico tropic hormone
 XX

PS Claim 2; Fig 4A; 94pp; English.

CC The invention relates to a modified protein selected from urocortin II
 CC (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
 CC composition is useful for treating a pathophysiological state including
 CC high body temperature, appetite dysfunction, congestive heart failure,
 CC stress, anxiety and undestirably low levels of adrenocortico tropic
 CC hormone (ACTH) secretions. A modified protein conjugate is useful in
 CC scintigraphy and in various assays. A modified protein conjugate is useful in
 CC destruction of Corticotropin-releasing factor (CRF) receptor bearing
 CC cells. The present sequence is mouse urocortin II (uon) protein.

SO Sequence 112 AA;

Query Match 54.18; Score 312; DB 23; Length 112;
 Best Local Similarity 60.9%; Pred. No. 2.1e-23;

Matches 67; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 1 MTRCALLLWLMGRVLYVPTPTPTQLRPNQSPOTPRPAASESPAATWMAAQS 60
 Db 1 MTRMALVVEVYVLMRLFPVGPPTPTFOLLPNQSLTETPSSVTSESSGTTTGPSAWS 60
 QY 61 HCSPTRHPSRIVSLDVPVIGLQILLEQARARAREQATTNARIARVG 110
 Db 61 NSKASPYLDTRVLTSLDVPVIGLRLTLEQARYARARQATNAQIIAHVG 110

RESULT 4
 AAE21007

ID AAE21007 standard; peptide; 41 AA.

AC AAE21007;

DT 01-JUL-2002 (first entry)

DE Human mature urocortin-related peptide (URP).

KW Human; urocortin-related peptide; URP; antipyretic; cardiant; urocortin;
 KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
 KW stress; anxiety.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Modified-site 41 /note= "C-terminal amide"

PN WO200212307-A1.

PD 14-FEB-2002.

PF 31-JUL-2001; 2001WO-US23976.

PR 04-AUG-2000; 2000US-223255P.

PR 07-MAR-2001; 2001US-273969P.

PA (RERE-) RES DEV FOUND.

PI Vale MW, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
 PI Hogenesch JB, Perrin MH;

DR WPI: 2002-241737/29.
 DR N-PSDB; AAD33401.

XX Novel urocortin II polypeptide or human urocortin-related peptide, for
 PT treating high body temperature, appetite dysfunction, congestive heart
 PT failure, stress, anxiety and low levels of adrenocortico tropic hormone
 XX

PS Claim 26; Page 30; 94pp; English.

CC The invention relates to a modified protein selected from urocortin II
 CC (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
 CC composition is useful for treating a pathophysiological state including
 CC high body temperature, appetite dysfunction, congestive heart failure,
 CC stress, anxiety and undestirably low levels of adrenocortico tropic
 CC hormone (ACTH) secretions. A modified protein conjugate is useful in
 CC scintigraphy and in various assays. A modified protein conjugate is useful in
 CC destruction of Corticotropin-releasing factor (CRF) receptor bearing
 CC cells. The present sequence is mature human URP.

SO Sequence 41 AA;

Query Match 34.08; Score 196; DB 23; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e-12;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 IVLSDDVPVIGLQILLEQARARAREQATTNARIARVGHG 112
 Db 1 IVLSDDVPVIGLQILLEQARARAREQATTNARIARVGHG 41

RESULT 5
 AAE21009

ID AAE21009 standard; peptide; 38 AA.

AC AAE21009;

DT 01-JUL-2002 (first entry)

DE Human urocortin-related peptide (URP).

KW Human; urocortin-related peptide; URP; antipyretic; cardiant; urocortin;
 KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
 KW stress; anxiety.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Modified-site 38 /note= "C-terminal amide"

PN WO200212307-A1.

PD 14-FEB-2002.

PF 31-JUL-2001; 2001WO-US23976.

PR 04-AUG-2000; 2000US-223255P.

PR 07-MAR-2001; 2001US-273969P.

PA (RERE-) RES DEV FOUND.

PI Vale MW, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
 PI Hogenesch JB, Perrin MH;

DR WPI: 2002-241737/29.

XX Novel urocortin II polypeptide or human urocortin-related peptide, for
 PT treating high body temperature, appetite dysfunction, congestive heart
 PT failure, stress, anxiety and low levels of adrenocortico tropic hormone
 XX

PS Claim 36; Fig 4b; 94pp; English.

CC The invention relates to a modified protein selected from urocortin II

PF 10-OCT-2001; 2001WO-US32065.
 XX
 PR 26-OCT-2000; 2000US-244128P.
 PR 15-MAR-2001; 2001US-27615P.
 XX
 PA (STRD) UNIV LEIAND STANFORD JUNIOR.
 XX
 PI Hsu SY, Hsueh AJW;
 XX
 DR WPI: 2002-471444/50.
 DR N-PSDB: AALA3490.
 XX
 PT Composition comprising human stresscopin 1 or stresscopin 2
 PT polypeptide, useful in appetite suppression, for cardioprotection,
 PT reducing edema, reducing inflammation, organ graft rejection, reducing
 PT hypertension
 XX
 PS Claim 2; Fig 1A; 50pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of two human
 CC proteins which activate the corticotropin releasing hormone receptor 2
 CC (CRH-R2). The proteins of the invention are called stresscopin 1 and
 CC stresscopin 2. The stresscopin DNA and protein sequences of the invention
 CC are useful for appetite suppression, cardioprotection, reducing oedema,
 CC reducing inflammation, reducing organ graft rejection, reducing
 CC hypertension and reducing trauma stress. The stresscopin DNA and protein
 CC sequences are also useful for the treatment of dysthymia, skin diseases,
 CC inflammatory arthritis, non-infectious inflammatory arthropathy (e.g.,
 CC rheumatoid arthritis), heart disease and stress-related disorders. The
 CC present amino acid sequence represents the human stresscopin 1 protein.
 XX
 SQ Sequence 112 AA;
 Query Match 100.0%; Score 577; DB 23; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.3e-49;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTRCALLLWMLGRVLYVPTPTPTQLRPNSSPOTTPRPAASESPSAPTWMAQS 60
 DB 1 MTRCALLLWMLGRVLYVPTPTPTQLRPNSSPOTTPRPAASESPSAPTWMAQS 60
 QY 61 HCSPTRHGSRIVSLDVPICGLDITLLEQARARAREQATNARILARVGHG 112
 DB 61 HCSPTRHGSRIVSLDVPICGLDITLLEQARARAREQATNARILARVGHG 112
 RESULT 2
 AAE21006
 ID AAE21006 standard; Protein; 112 AA.
 XX
 AC AAE21006;
 XX
 DT 01-JUL-2002 (first entry)
 DE Human urocortin-related peptide (URP) protein.
 KW Human; urocortin-related peptide; URP; antipyretic; cardiast; urocortin;
 KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
 KW stress; anxiety.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= Signal_peptide
 FT 72..112
 FT /label= Mature_URP_protein
 FT Modified-site 112
 FT /note= "C-terminal amide"
 XX
 PN WO200212307-A1.
 XX
 PD 14-FEB-2002.

XX
 PF 31-JUL-2001; 2001WO-US23976.
 XX
 PR 04-AUG-2000; 2000US-223255P.
 PR 07-MAR-2001; 2001US-273969P.
 XX
 PA (RERE-) RES DEV FOUND.
 XX
 PI Vale WM, Sawchenko PF, Lewis KA, Vaughan JM, Reyes TM, Rivier JE;
 PI Hogenesch JB, Perrin MH;
 XX
 DR WPI: 2002-241737/29.
 DR N-PSDB: AMD33401.
 XX
 PT Novel urocortin II polypeptide or human urocortin-related peptide, for
 PT treating high body temperature, appetite dysfunction, congestive heart
 PT failure, stress, anxiety and low levels of adrenocortico tropic hormone
 PT
 XX
 PS Claim 18; Fig 1; 94pp; English.
 XX
 CC The invention relates to a modified protein selected from urocortin II
 CC (Ucn II) and human urocortin-related peptide (URP). A pharmaceutical
 CC composition is useful for treating a pathophysiological state including
 CC high body temperature, appetite dysfunction, congestive heart failure,
 CC stress, anxiety and undestirably low levels of adrenocortico tropic
 CC hormone (ACTH) secretions. A modified protein conjugate is useful in
 CC scintigraphy and in various assays, and also for the targeted
 CC destruction of corticotropin-releasing factor (CRF) receptor bearing
 CC cells. The present sequence is human URP protein.
 XX
 SQ Sequence 112 AA;
 Query Match 100.0%; Score 577; DB 23; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.3e-49;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTRCALLLWMLGRVLYVPTPTPTQLRPNSSPOTTPRPAASESPSAPTWMAQS 60
 DB 1 MTRCALLLWMLGRVLYVPTPTPTQLRPNSSPOTTPRPAASESPSAPTWMAQS 60
 QY 61 HCSPTRHGSRIVSLDVPICGLDITLLEQARARAREQATNARILARVGHG 112
 DB 61 HCSPTRHGSRIVSLDVPICGLDITLLEQARARAREQATNARILARVGHG 112
 RESULT 3
 AAE21008
 ID AAE21008 standard; Protein; 112 AA.
 XX
 AC AAE21008;
 XX
 DT 01-JUL-2002 (first entry)
 DE Mouse urocortin II (ucn) protein.
 KW Mouse; urocortin-related peptide; URP; antipyretic; cardiast; urocortin;
 KW ucn; tranquilliser; appetite dysfunction; congestive heart failure;
 KW stress; anxiety.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= Signal_peptide
 FT 72..112
 FT /label= Mature_URP_protein
 FT Modified-site 112
 FT /note= "C-terminal amide"
 XX
 PN WO200212307-A1.
 XX
 PD 14-FEB-2002.
 XX
 PF 31-JUL-2001; 2001WO-US23976.
 XX
 PR 04-AUG-2000; 2000US-223255P.
 PR 07-MAR-2001; 2001US-273969P.
 XX
 PA (RERE-) RES DEV FOUND.
 XX

XX PD

Drosophila melanogaster
Mycobacterium spec
Mycobacterium spec
Propionibacterium
Eucalyptus grandis
Drosophila melanogaster
Human ovarian anti
mycobacterium tube
mycobacterium tube
Fibronectin attach
Mycobacterium tube
Mycobacterium tube
mycobacterium tube
Mⁱ. tuberculosis Im
MycoBacterium tube
M. tuberculosis re
M. tuberculosis DP
Mycobacterium spec
Truncated cellulase
Active cellulase p
Human polyprotein
Drosophila melanogaster
peptide #6950 enco
Protein #6208 enco
Human brain expres
Human bone marrow
Peptide #7010 enco
Human peptide enco
Human polypeptide
Arabidopsis thaliana
Herbicidally active
C glutamicum proteo
Human novel secret
Mycobacterium spec

Tue Mar 25 08:25:19 2003

us-09-682-706-2.rapb

Page 1

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: March 21, 2003, 11:59:59 ; Search time 17.3419 Seconds

(without alignments)
345,277 Million cell updates/sec

Title: US-09-682-706-2

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Total number of hits satisfying chosen parameters: 221153

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2-6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
5: /cgn2-6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
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14: /cgn2-6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	577	100.0	112	10	US-09-919-473-2
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4	196	34.0	41	10	US-09-919-473-3
5	191	33.1	43	10	US-09-682-706-3
6	173	30.0	38	9	US-10-099-766-6
7	173	30.0	38	10	US-09-919-473-4
8	139	24.1	38	9	US-10-099-766-9
9	139	24.1	38	10	US-09-919-473-11
10	96.5	16.7	161	9	US-10-099-766-2
11	96.5	16.7	161	10	US-09-682-706-5
12	95	16.5	40	10	US-09-682-706-15
13	89	15.4	164	9	US-10-099-766-4
14	86	14.9	38	9	US-10-099-766-6
15	86	14.9	38	10	US-09-919-473-12
16	83	14.4	357	9	US-09-809-391-755
17	82	14.2	40	10	US-09-682-706-6
18	81	14.0	124	9	US-09-818-009-15
19	80	13.9	38	9	US-10-099-766-7

20	79	13.7	38	9	US-10-099-766-3	Sequence 3, Appli
21	77.5	13.4	113	10	US-09-864-761-39507	Sequence 39507, A
22	77	13.3	75	9	US-09-738-626-6321	Sequence 6321, Ap
23	76.5	13.3	244	10	US-09-764-864-1111	Sequence 1111, Ap
24	75.5	13.1	77	9	US-09-776-724A-87	Sequence 87, Appli
25	74	12.8	562	10	US-09-981-900B-5	Sequence 5, Appli
26	73.5	12.7	128	9	US-09-738-626-5866	Sequence 5866, Ap
27	72.5	12.7	458	10	US-09-796-753-18	Sequence 18, Appli
28	72.5	12.6	329	10	US-09-764-864-1059	Sequence 1059, Ap
29	72.5	12.6	329	10	US-09-764-864-1482	Sequence 1482, Ap
30	72	12.5	38	9	US-10-099-766-5	Sequence 5, Appli
31	72	12.5	559	10	US-09-858-155A-2	Sequence 2, Appli
32	71.5	12.4	1023	9	US-09-893-519A-14	Sequence 14, Appli
33	71.5	12.4	2783	10	US-09-816-669A-14	Sequence 14, Appli
34	71	12.3	101	10	US-09-867-550-1536	Sequence 1536, Ap
35	71	12.3	3635	9	US-10-037-182-4	Sequence 4, Appli
36	71	12.3	3635	10	US-09-845-583-2	Sequence 2, Appli
37	70.5	12.2	109	9	US-09-738-626-4916	Sequence 4916, Ap
38	70.5	12.2	197	10	US-09-816-095-5	Sequence 5, Appli
39	70.5	12.2	205	9	US-09-809-391-502	Sequence 502, App
40	70.5	12.2	258	10	US-09-925-302-656	Sequence 656, App
41	70.5	12.2	323	10	US-09-816-095-2	Sequence 2, Appli
42	70	12.1	231	10	US-09-925-301-1210	Sequence 1210, Ap
43	70	12.1	344	10	US-09-771-161A-173	Sequence 173, App
44	70	12.1	684	10	US-09-823-240-9	Sequence 9, Appli
45	70	12.1	712	10	US-09-773-753-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-682-706-2
Sequence 2, Application US/09682706
Patent No. US20020082409A1
GENERAL INFORMATION:
APPLICANT: Hsu, Sheau-Yu
TITLE OF INVENTION: Stresscopins and their ses
FILE REFERENCE: STAN210
CURRENT APPLICATION NUMBER: US/09/682,706
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/276,615
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/244,128
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 112
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-682-706-2

Query Match 100.0%; Score 577; DB 10; Length 112;
Best Local Similarity 100.0%; Pred. No. 3e+6;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCALLLMVLMGRVLYVPTPTPTOLRONSPOQTTPRAASPSAATWPAAS 60
DB 1 MTRCALLLMVLMGRVLYVPTPTPTOLRONSPOQTTPRAASPSAATWPAAS 60

QY 61 HCSPTRRHGSRTVLSLDVPIGLIQLLEQARARAREQTNNRIARVGHG 112
DB 61 HCSPTRRHGSRTVLSLDVPIGLIQLLEQARARAREQTNNRIARVGHG 112

RESULT 2
US-09-919-473-2
Sequence 2, Application US/09919473
Patent No. US20020127221A1
GENERAL INFORMATION:
APPLICANT: Vale, Wylie Walker Jr.

Yes, seq ID 2 is present.

```

; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Eouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Urocortin-related peptide (hURP)
; US-09-919-473-2

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Query Match          100.0%; Score 577; DB 10; Length 112;
Best Local Similarity 100.0%; Pred. No. 3e-46;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MTRCALLLVMLGRLVVPVPTPTFQLRPNQSPQTPRPAASESPSAAPTPWMAQS 60
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DB 1 MTRCALLLVMLGRLVVPVPTPTFQLRPNQSPQTPRPAASESPSAAPTPWMAQS 60
QY 61 HCSPTRHGSRIVLSLDPVIGLQILLEQARARAREQATTNARIARVGHG 112
    |||||
DB 61 HCSPTRHGSRIVLSLDPVIGLQILLEQARARAREQATTNARIARVGHG 112

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RESULT 3
US-09-919-473-10
; Sequence 10, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Eouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Mouse Urocortin II precursor peptide
; US-09-919-473-10

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Query Match          54.1%; Score 312; DB 10; Length 112;
Best Local Similarity 60.9%; Pred. No. 6.1e-22;
Matches 67; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

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QY 1 MTRCALLLVMLGRLVVPVPTPTFQLRPNQSPQTPRPAASESPSAAPTPWMAQS 60
    |||||
DB 1 MTRCALLLVMLGRLVVPVPTPTFQLRPNQSPQTPRPAASESPSAAPTPWMAQS 60
QY 61 HCSPTRHGSRIVLSLDPVIGLQILLEQARARAREQATTNARIARVGHG 110
    |||||

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DB 61 NSKASPTLDTIVLSLDPVIGLQILLEQARARAREQATTNARIARVGHG 110
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RESULT 4
US-09-919-473-3
; Sequence 3, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Eouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 3
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Urocortin-related peptide (hURP)
; US-09-919-473-3

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Query Match          34.0%; Score 196; DB 10; Length 41;
Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 72 IVSLDVPVIGLQILLEQARARAREQATTNARIARVGHG 112
    |||||
DB 1 IVSLDVPVIGLQILLEQARARAREQATTNARIARVGHG 41
    |||||

```

```

RESULT 5
US-09-682-706-3
; Sequence 3, Application US/09682706
; Patent No. US20020082409A1
; GENERAL INFORMATION:
; APPLICANT: Hsueh, Aaron
; APPLICANT: Hsueh, Aaron
; TITLE OF INVENTION: Stresscopins and their ses
; FILE REFERENCE: STANZ10
; CURRENT APPLICATION NUMBER: US/09/682,706
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/276,615
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/244,128
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-682-706-3

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Query Match          33.1%; Score 191; DB 10; Length 43;
Best Local Similarity 95.3%; Pred. No. 2.7e-11;
Matches 41; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 67 HPGSRIVLSLDPVIGLQILLEQARARAREQATTNARIARV 109
    |||||
DB 1 HPGSRIVLSLDPVIGLQILLEQARARAREQATTNARIARV 43
    |||||

```

RESULT 6

US-10-099-766-8
; Sequence 8, Application US/10099766
; Publication No. US20030036507A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Kathy
; APPLICANT: Vale, Wylie
; APPLICANT: Marilyn H. Perrin
; APPLICANT: Jean E. Rivier
; APPLICANT: Joszef Gulyas
; APPLICANT: Koichi S. Kunitake
; TITLE OF INVENTION: Urocortin III and Uses Thereof
; FILE REFERENCE: D6390
; CURRENT APPLICATION NUMBER: US/10/099,766
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/276,069
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 8
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human urocortin-related peptide (hURP),
US-10-099-766-8

Query Match 30.0%; Score 173; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1,1e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 IVLSIDVPIGLILLEQARARAREQATTNARIARY 109
DB 1 IVLSIDVPIGLILLEQARARAREQATTNARIARY 38

RESULT 7

US-09-919-473-4
; Sequence 4, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 4
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acids 1-38 of human
; OTHER INFORMATION: Urocortin-related peptide (hURP)
US-09-919-473-4

Query Match 30.0%; Score 173; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 1,1e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 IVLSIDVPIGLILLEQARARAREQATTNARIARY 109
DB 1 IVLSIDVPIGLILLEQARARAREQATTNARIARY 38

RESULT 8

US-10-099-766-9
; Sequence 9, Application US/10099766
; Publication No. US20030036507A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Kathy
; APPLICANT: Vale, Wylie
; APPLICANT: Marilyn H. Perrin
; APPLICANT: Jean E. Rivier
; APPLICANT: Koichi S. Kunitake
; APPLICANT: Joszef Gulyas
; TITLE OF INVENTION: Urocortin III and Uses Thereof
; FILE REFERENCE: D6390
; CURRENT APPLICATION NUMBER: US/10/099,766
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/276,069
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 9
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Mouse urocortin II (mUcn II)
US-10-099-766-9

Query Match 24.1%; Score 139; DB 9; Length 38;
Best Local Similarity 76.3%; Pred. No. 1,4e-06;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 72 IVLSIDVPIGLILLEQARARAREQATTNARIARY 109
DB 1 IVLSIDVPIGLILLEQARARAREQATTNARIARY 38

RESULT 9

US-09-919-473-11
; Sequence 11, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Mouse urocortin II
US-09-919-473-11

Query Match 24.1%; Score 139; DB 10; Length 38;
Best Local Similarity 76.3%; Pred. No. 1,4e-06;
Matches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 72 IVLSIDVPIGLILLEQARARAREQATTNARIARY 109
DB 1 IVLSIDVPIGLILLEQARARAREQATTNARIARY 38

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RESULT 10
US-10-099-766-2
; Sequence 2, Application US/10099766
; Publication No. US20030036507A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Kathy
; APPLICANT: Vale, Wylie
; APPLICANT: Marilyn H. Perrin
; APPLICANT: Jean E. Rivier
; APPLICANT: Joseph S. Kunitake
; APPLICANT: Jozsef Gulyas
; TITLE OF INVENTION: Urocortin III and Uses Thereof
; FILE REFERENCE: D6390
; CURRENT APPLICATION NUMBER: US/10/099,766
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 60/276,069
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 2
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Human urocortin III Precursor
US-10-099-766-2

Query Match          16.7%; Score 96.5; DB 9; Length 161;
Best Local Similarity 28.2%; Pred. No. 0.052;
Matches 22; Conservative 14; Mismatches 23; Indels 19; Gaps 1;

QY 33 QNSPQTTTPRAASESPSAFTWPAQSHCSPTFRHSGRIYLSLDVPIGLQILLEGQARA 92
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 100 QAQPRGKPRQDTAKSPHR-----TKFTLSLDVPTNIMNLEFNIAKA 140

QY 93 RAAREQATTNARIARVG 110
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 141 KNLRQAQANAHMAOIG 158

RESULT 11
US-09-682-706-5
; Sequence 5, Application US/09682706
; Patent No. US20020082409A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Sheau-Yu
; APPLICANT: Hsueh, Aaron
; TITLE OF INVENTION: Stressoscops and their ses
; FILE REFERENCE: STAN210
; CURRENT APPLICATION NUMBER: US/09/682,706
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/276,615
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/244,128
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-682-706-5

Query Match          16.7%; Score 96.5; DB 10; Length 161;
Best Local Similarity 28.2%; Pred. No. 0.052;
Matches 22; Conservative 14; Mismatches 23; Indels 19; Gaps 1;

QY 33 QNSPQTTTPRAASESPSAFTWPAQSHCSPTFRHSGRIYLSLDVPIGLQILLEGQARA 92
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 100 QAQPRGKPRQDTAKSPHR-----TKFTLSLDVPTNIMNLEFNIAKA 140

QY 93 RAAREQATTNARIARVG 110
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 141 KNLRQAQANAHMAOIG 158
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RESULT 12
US-09-682-706-15
; Sequence 15, Application US/09682706
; Patent No. US20020082409A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Sheau-Yu
; APPLICANT: Hsueh, Aaron
; TITLE OF INVENTION: Stressoscops and their ses
; FILE REFERENCE: STAN210
; CURRENT APPLICATION NUMBER: US/09/682,706
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/276,615
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/244,128
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Takifugu rubripes
US-09-682-706-15

Query Match          16.5%; Score 95; DB 10; Length 40;
Best Local Similarity 45.0%; Pred. No. 0.016;
Matches 18; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 70 SRIVSLDVPIGLQILLEGQARAAREQATTNARIARV 109
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 SRTLISLDVPTNIMNIFDVAKAKNLRKAENARLLAHI 40

RESULT 13
US-10-099-766-4
; Sequence 4, Application US/10099766
; Publication No. US20030036507A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Kathy
; APPLICANT: Vale, Wylie
; APPLICANT: Marilyn H. Perrin
; APPLICANT: Jean E. Rivier
; APPLICANT: Joseph S. Kunitake
; APPLICANT: Jozsef Gulyas
; TITLE OF INVENTION: Urocortin III and Uses Thereof
; FILE REFERENCE: D6390
; CURRENT APPLICATION NUMBER: US/10/099,766
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/276,069
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 4
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Mouse urocortin III Precursor
US-10-099-766-4

Query Match          15.4%; Score 89; DB 9; Length 164;
Best Local Similarity 36.2%; Pred. No. 0.26;
Matches 17; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 64 PTRHSGRIYLSLDVPIGLQILLEGQARAAREQATTNARIARVG 110
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 115 PKSDRGKFTLSLDVPTNIMNIFDVAKAKNLRKAENARLLAHI 161

RESULT 14
US-10-099-766-6
; Sequence 6, Application US/10099766
; Publication No. US20030036507A1
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Tue Mar 25 08:25:24 2003

us-09-682-706-3.rapb

Page 1

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: March 21, 2003, 11:59:59 ; Search time 6.65806 Seconds

(without alignments)
345.277 Million cell updates/sec

Title: US-09-682-706-3

Perfect score: 200

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Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications: AA:*
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3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	191	95.5	112	10	US-09-682-706-2
4	161	80.5	38	9	US-10-099-766-8
5	161	80.5	38	10	US-09-919-473-4
6	161	80.5	41	10	US-09-919-473-3
7	133	66.5	112	10	US-09-919-473-10
8	127	63.5	38	9	US-10-099-766-9
9	127	63.5	38	10	US-09-919-473-11
10	85	42.5	40	10	US-09-682-706-15
11	76	38.0	38	9	US-10-099-766-6
12	76	38.0	38	10	US-09-919-473-12
13	72	36.0	40	10	US-09-682-706-6
14	72	36.0	161	9	US-10-099-766-2
15	72	36.0	161	10	US-09-682-706-5
16	71	35.5	164	9	US-10-099-766-4
17	70	35.0	38	9	US-10-099-766-7
18	69	34.5	38	9	US-10-099-766-3
19	63	31.5	40	9	US-09-818-009-8

20	63	31.5	40	9	US-10-099-766-14
21	63	31.5	40	9	US-10-099-766-15
22	63	31.5	40	10	US-09-919-473-5
23	63	31.5	40	10	US-09-919-473-13
24	63	31.5	40	10	US-09-997-498-10
25	63	31.5	40	10	US-09-997-498-11
26	63	31.5	41	9	US-09-818-009-17
27	63	31.5	42	10	US-09-682-706-9
28	63	31.5	42	10	US-09-682-706-10
29	63	31.5	124	9	US-09-818-009-15
30	62	31.0	38	9	US-10-099-766-5
31	62	31.0	41	9	US-09-818-009-3
32	61	30.5	41	9	US-09-818-009-4
33	61	30.5	41	9	US-10-099-766-10
34	61	30.5	41	10	US-09-919-473-6
35	61	30.5	41	10	US-09-997-498-1
36	61	30.5	41	10	US-09-997-498-2
37	61	30.5	42	10	US-09-682-706-7
38	61	30.5	196	10	US-09-853-386-104
39	60	30.0	41	9	US-09-818-009-4
40	60	30.0	41	9	US-09-818-009-7
41	60	30.0	41	10	US-09-997-498-3
42	60	30.0	41	10	US-09-997-498-6
43	60	30.0	41	10	US-09-997-498-7
44	60	30.0	42	10	US-09-682-706-12
45	59	29.5	41	9	US-09-818-009-5

ALIGNMENTS

RESULT 1
US-09-682-706-3
Sequence 3, Application US/09682706
Patent No. US20020082409A1
GENERAL INFORMATION:
APPLICANT: Hsu, Sheau-Yu
TITLE OF INVENTION: Stresscopins and their ses
FILE REFERENCE: STAN210
CURRENT APPLICATION NUMBER: US/09/682,706
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/276,615
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/244,128
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
US-09-682-706-3

Query Match 100.0% Score 200: DB 10: Length 43:
Best Local Similarity 100.0% Pred. No. 1.1e-21:
Matches 43: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

DB 1 HPGSRIVSLDVILGLILQTLLEQARRAREQATTNARILARY 43
1 HPGSRIVSLDVILGLILQTLLEQARRAREQATTNARILARY 43

RESULT 2
US-09-682-706-2
Sequence 2, Application US/09682706
Patent No. US20020082409A1
GENERAL INFORMATION:
APPLICANT: Hsu, Sheau-Yu
TITLE OF INVENTION: Stresscopins and their ses
FILE REFERENCE: STAN210
CURRENT APPLICATION NUMBER: US/09/682,706

```
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/276,615
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/244,128
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-682-706-2
```

```
Query Match          95.5%; Score 191; DB 10; Length 112;
Best Local Similarity 95.3%; Pred. No. 6.8e-20;
Matches 41; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 HPGSRIVSLDVIIGLQILLEQARARAREQATTNARIARV 43
DB 67 HPGSRIVSLDVIIGLQILLEQARARAREQATTNARIARV 109
```

```
RESULT 3
US-09-919-473-2
```

```
; Sequence 2, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
; TITLE OF INVENTION: Urocortlin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Urocortlin-related peptide (hURP)
; OTHER INFORMATION: precursor peptide
; US-09-919-473-2
```

```
Query Match          95.5%; Score 191; DB 10; Length 112;
Best Local Similarity 95.3%; Pred. No. 6.8e-20;
Matches 41; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
DB 1 HPGSRIVSLDVIIGLQILLEQARARAREQATTNARIARV 43
67 HPGSRIVSLDVIIGLQILLEQARARAREQATTNARIARV 109
```

```
RESULT 4
US-10-099-766-8
```

```
; Sequence 8, Application US/10099766
; Publication No. US20030036507A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Kathy
; APPLICANT: Vale, Wylie
; APPLICANT: Marilyn H. Perrin
; APPLICANT: Jean E. Rivier
; APPLICANT: Koichi S. Kunitake
; APPLICANT: Josef Gulyas
; TITLE OF INVENTION: Urocortlin III and Uses Thereof
; FILE REFERENCE: D6390
```

```
; CURRENT APPLICATION NUMBER: US/10/099,766
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/276,069
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 8
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Urocortlin-related peptide (hURP),
; OTHER INFORMATION: human urocortlin II
; US-10-099-766-8
```

```
Query Match          80.5%; Score 161; DB 9; Length 38;
Best Local Similarity 94.7%; Pred. No. 3.1e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 IVLSLDVPIGLQILLEQARARAREQATTNARIARV 43
DB 1 IVLSLDVPIGLQILLEQARARAREQATTNARIARV 38
```

```
RESULT 5
US-09-919-473-4
```

```
; Sequence 4, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
; TITLE OF INVENTION: Urocortlin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 4
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acids 1-38 of human
; OTHER INFORMATION: Urocortlin-related peptide (hURP)
; US-09-919-473-4
```

```
Query Match          80.5%; Score 161; DB 10; Length 38;
Best Local Similarity 94.7%; Pred. No. 3.1e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 IVLSLDVPIGLQILLEQARARAREQATTNARIARV 43
DB 1 IVLSLDVPIGLQILLEQARARAREQATTNARIARV 38
```

```
RESULT 6
US-09-919-473-3
```

```
; Sequence 3, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
```



```
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 3
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Urocortin-related peptide (hurrp)
S-09-919-473-3
```

```
Query Match      80.5%; Score 161; DB 10; Length 41;
Best Local Similarity 94.7%; Pred. No. 3.4e-16;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 IVLSDVILGLQILLEGQARARAEQATTNARIARV 43
DB 1 IVLSDVPIGLILLEGQARARAEQATTNARIARV 38
```

```
RESULT 7
US-09-919-473-10
; Sequence 10, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Mouse Urocortin II precursor peptide
US-09-919-473-10
```

```
Query Match      66.5%; Score 133; DB 10; Length 112;
Best Local Similarity 70.0%; Pred. No. 1.1e-11;
Matches 28; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 4 SRIVSLDVILGLQILLEGQARARAEQATTNARIARV 43
DB 70 TRVILSLDVPIGLILLEGQARARAEQATTNARIARV 109
```

```
RESULT 8
US-10-099-766-9
; Sequence 9, Application US/10099766
; Publication No. US20030036507A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Kathy
; APPLICANT: Vale, Wylie
; APPLICANT: Marilyn H. Perrin
; APPLICANT: Jean E. Rivier
; APPLICANT: Koichi S. Kunitake
; APPLICANT: Jozsef Gulyas
```

```
; TITLE OF INVENTION: Urocortin III and Uses Thereof
; FILE REFERENCE: D6390
; CURRENT APPLICATION NUMBER: US/10/099,766
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/276,069
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 9
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Mouse Urocortin II (mucn II)
US-10-099-766-9
```

```
Query Match      63.5%; Score 127; DB 9; Length 38;
Best Local Similarity 71.1%; Pred. No. 2e-11;
Matches 27; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 6 IVLSDVILGLQILLEGQARARAEQATTNARIARV 43
DB 1 VIIISDVPIGLILLEGQARARAEQATTNARIARV 38
```

```
RESULT 9
US-09-919-473-11
; Sequence 11, Application US/09919473
; Patent No. US20020127221A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie Walker Jr.
; APPLICANT: Lewis, Kathy Ann
; APPLICANT: Reyes, Teresa Marie
; APPLICANT: Hogenesch, John Beren
; APPLICANT: Sawchenko, Paul Emil
; APPLICANT: Vaughan, Joan Maureen
; APPLICANT: Rivier, Jean Edouard Frederic
; APPLICANT: Perrin, Marilyn Heller
; TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
; FILE REFERENCE: D6334
; CURRENT APPLICATION NUMBER: US/09/919,473
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/273,969
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 11
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Mouse Urocortin II
US-09-919-473-11
```

```
Query Match      63.5%; Score 127; DB 10; Length 38;
Best Local Similarity 71.1%; Pred. No. 2e-11;
Matches 27; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 6 IVLSDVILGLQILLEGQARARAEQATTNARIARV 43
DB 1 VIIISDVPIGLILLEGQARARAEQATTNARIARV 38
```

```
RESULT 10
US-09-682-706-15
; Sequence 15, Application US/09682706
; Patent No. US20020082409A1
; GENERAL INFORMATION:
; APPLICANT: Hsueh, Aaron
; APPLICANT: Stan210
; TITLE OF INVENTION: Stresscopsins and their ses
; FILE REFERENCE: STAN210
; CURRENT APPLICATION NUMBER: US/09/682,706
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/276,615
```

PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/244,128
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 40
TYPE: PRT
ORGANISM: Takifugu rubripes
US-09-682-706-15

Query Match 42.5%; Score 85; DB 10; Length 40;
Best Local Similarity 42.5%; Pred. No. 1.8e-05;
Matches 17; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 4 SRIVSLDVILGLQILLEQARARAREQATTNARIARV 43
DB 1 LTLSDVPTNIMNVLEFDVAKAKMLRAKKAENARLAIH 40

RESULT 11
US-10-099-766-6
Sequence 6, Application US/10099766
Publication No. US20030036507A1
GENERAL INFORMATION:
APPLICANT: Lewis, Kathy
APPLICANT: Vale, Wylie
APPLICANT: Marilyn H. Perrin
APPLICANT: Jean E. Rivier
APPLICANT: Koichi S. Kunitake
APPLICANT: Josef Gulyas
TITLE OF INVENTION: Urocortin III and Uses Thereof
FILE REFERENCE: D6390
CURRENT APPLICATION NUMBER: US/10/099,766
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/276,069
PRIOR FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 6
LENGTH: 38
TYPE: PRT
ORGANISM: Takifugu rubripes
FEATURE:
OTHER INFORMATION: Pufferfish Urocortin Related Peptide
US-10-099-766-6

Query Match 38.0%; Score 76; DB 9; Length 38;
Best Local Similarity 39.5%; Pred. No. 0.00033;
Matches 15; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 6 IVLSLDVILGLQILLEQARARAREQATTNARIARV 43
DB 1 LTLSDVPTNIMNVLEFDVAKAKMLRAKKAENARLAIH 38

RESULT 12
US-09-919-473-12
Sequence 12, Application US/09919473
Patent No. US20020127221A1
GENERAL INFORMATION:
APPLICANT: Vale, Wylie Walker Jr.
APPLICANT: Lewis, Kathy Ann
APPLICANT: Reyes, Teresa Marie
APPLICANT: Hogenesch, John Beren
APPLICANT: Sawchenko, Paul Emil
APPLICANT: Vaughan, Joan Maureen
APPLICANT: Rivier, Jean Edouard Frederic
APPLICANT: Perrin, Marilyn Heller
TITLE OF INVENTION: Urocortin Proteins and Uses Thereof
FILE REFERENCE: D6334
CURRENT APPLICATION NUMBER: US/09/919,473
CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 60/273,969
PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 12
LENGTH: 38
TYPE: PRT
ORGANISM: Takifugu rubripes
FEATURE:
OTHER INFORMATION: Pufferfish Urocortin Related Peptide
US-09-919-473-12

Query Match 38.0%; Score 76; DB 10; Length 38;
Best Local Similarity 39.5%; Pred. No. 0.00033;
Matches 15; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 6 IVLSLDVILGLQILLEQARARAREQATTNARIARV 43
DB 1 LTLSDVPTNIMNVLEFDVAKAKMLRAKKAENARLAIH 38

RESULT 13
US-09-682-706-6
Sequence 6, Application US/09682706
Patent No. US20020082409A1
GENERAL INFORMATION:
APPLICANT: Hsu, Sheau-Yu
APPLICANT: Hsueh, Aaron
TITLE OF INVENTION: Stresscopsins and their ses
FILE REFERENCE: STAN210
CURRENT APPLICATION NUMBER: US/09/682,706
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/276,615
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/244,128
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-09-682-706-6

Query Match 36.0%; Score 72; DB 10; Length 40;
Best Local Similarity 35.0%; Pred. No. 0.0013;
Matches 14; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 4 SRIVSLDVILGLQILLEQARARAREQATTNARIARV 43
DB 1 TKFTLSLDVPTNIMNVLEFNIAKAKMLRAQAAANHLMAQI 40

RESULT 14
US-10-099-766-2
Sequence 2, Application US/10099766
Publication No. US20030036507A1
GENERAL INFORMATION:
APPLICANT: Lewis, Kathy
APPLICANT: Vale, Wylie
APPLICANT: Marilyn H. Perrin
APPLICANT: Jean E. Rivier
APPLICANT: Koichi S. Kunitake
APPLICANT: Josef Gulyas
TITLE OF INVENTION: Urocortin III and Uses Thereof
FILE REFERENCE: D6390
CURRENT APPLICATION NUMBER: US/10/099,766
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/276,069
PRIOR FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 2
LENGTH: 161
TYPE: PRT

Tue Mar 25 08:25:24 2003

us-09-682-706-3.rapb

Page 5

ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: Human urocortin III Precursor
US-10-099-766-2

Query Match
Best Local Similarity 36.0%; Score 72; DB 9; Length 161;
Matches 14; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 4 SRIVLSLVYILGLQILILEQARARAREQATTNARIARY 43
DB 118 TKFTLSLDVPTNIMNLEFNIAKAKNLRQAANAHLMAOI 157

RESULT 15

US-09-682-706-5
Sequence 5, Application US/09682706
Patent No. US20020082409A1
GENERAL INFORMATION:

APPLICANT: Hsu, Sheau-Yu
APPLICANT: Hsueh, Aaron

TITLE OF INVENTION: Stresscopins and their ses

FILE REFERENCE: STAN210
CURRENT APPLICATION NUMBER: US/09/682,706

CURRENT FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/276,615

PRIOR FILING DATE: 2001-03-15

PRIOR APPLICATION NUMBER: 60/244,128

PRIOR FILING DATE: 2000-10-26

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 161

TYPE: PRT

ORGANISM: Homo sapiens

US-09-682-706-5
Query Match
Best Local Similarity 36.0%; Score 72; DB 10; Length 161;
Matches 14; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 4 SRIVLSLVYILGLQILILEQARARAREQATTNARIARY 43
DB 118 TKFTLSLDVPTNIMNLEFNIAKAKNLRQAANAHLMAOI 157

Search completed: March 21, 2003, 12:00:51
Job time : 6.65806 secs



GenCore version 5.1.4-P5-A578
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OM protein - protein search, using sw model

Run on: March 21, 2003, 11:56:43 ; Search time 11.5613 Seconds
(without alignments)
401.802 Million cell updates/sec

Title: us-09-682-706-2

Performance score: 577

Sequence: 1 MTRCALLLLNVLMLGRVLYV.....RAAREQATNARILARYGHC 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	577	100.0	112 1 UCN2_HUMAN	Q96RP3 homo sapien
2	314.5	54.5	109 1 UCN2_RAT	Q91W1L rattus norv
3	312	54.1	112 1 UCN2_MOUSE	Q99M18 mus musculu
4	96.5	16.7	161 1 UCN3_HUMAN	Q96963 homo sapien
5	89.5	15.5	122 1 UCN1_MOUSE	P61615 mus musculu
6	89	15.4	122 1 UCN1_RAT	P50990 rattus norv
7	89	15.4	164 1 UCN3_MOUSE	Q92444 mus musculu
8	81	14.0	124 1 UCN1_HUMAN	P55089 homo sapien
9	81	14.0	357 1 IF35_HUMAN	000303 homo sapien
10	79.5	13.8	3149 1 TEGU_EBV	P03186 epstein-bar
11	79	13.7	707 1 MM09_RABIT	P41246 onycholagus
12	78.5	13.6	325 1 MODD_MYCBO	Q30620 mycobacteri
13	78.5	13.6	325 1 MODD_MYCCTU	Q50906 mycobacteri
14	77.5	13.4	837 1 GC12_HUMAN	Q92830 homo sapien
15	76	13.2	279 1 Y091_NPYOP	O10341 oryza pseu
16	76	13.2	1113 1 MYSD_DICDI	P34109 dictyosteli
17	75.5	13.1	623 1 MUTL_BRME	O8YB74 bruceella
18	75	13.0	268 1 NO20_MEDTR	P93329 bruceella tr
19	75	13.0	837 1 MUC1_RAT	P98089 rattus norv
20	74	12.8	187 1 GUN1_RAT	P01143 rattus norv
21	74	12.8	562 1 GUN1_ACICE	P54583 acidotherru
22	73.5	12.7	162 1 CRF_XENLA	P49188 xenopus lae
23	73	12.7	235 1 AURB_CHLAU	P27197 chloroflexu
24	73	12.7	1507 1 Y056_HUMAN	P42685 homo sapien
25	73	12.7	1840 1 SUTS_RAT	P23739 rattus norv
26	72.5	12.6	122 1 CRF_CANFA	P49926 canis fami
27	72.5	12.6	1387 1 TROP_HUMAN	Q12816 homo saplen
28	72	12.5	191 1 CRF_PIG	P06296 sus scrofa
29	72	12.5	474 1 VTP3_TTVIV	P19275 thermoprote
30	72	12.5	558 1 PODX_HUMAN	Q00592 homo sapien
31	72	12.5	559 1 WAS1_HUMAN	Q92558 homo sapien
32	71.5	12.4	544 1 GP10_DICDI	Q06885 dictyosteli
33	71.5	12.4	585 1 PKNI_MYCTU	Q10964 mycobacteri

ALIGNMENTS

34	71.5	12.4	1083 1 T2D3_HUMAN	O00268 homo sapien
35	71.5	12.4	3703 1 ABP1_HUMAN	O15911 homo sapien
36	71.5	12.4	3726 1 ABP1_MOUSE	O61329 mus musculu
37	71	12.3	308 1 MACS_RAT	P30009 rattus norv
38	71	12.3	622 1 LAM0_BROME	P08928 drosophila
39	71	12.3	864 1 WS14_MOUSE	Q99m23 mus musculu
40	71	12.3	1742 1 GUNA_GALSA	P22534 caldocellum
41	71	12.3	3718 1 LMA5_MOUSE	O61001 mus musculu
42	70.5	12.2	126 1 PAHO_CAVPO	P13083 cavia porce
43	70.5	12.2	283 1 EXN1_SORBI	P24152 sorghum bic
44	70.5	12.2	323 1 B362_HUMAN	Q9np25 homo sapien
45	70.5	12.2	387 1 A2AB_MACPR	O19025 macroscellid

RESULT 1
UCN2_HUMAN
ID UCN2_HUMAN STANDARD: PRT: 112 AA.
AC Q96RP3; Q9BUC0; (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Urococtin II precursor (Ucn II) (stresscopin-related peptide)
DE (Urococtin-related peptide).
GN UCN2 OR SRP OR URP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RX MEDLINE=21227098; PubMed=11329063;
RA Hsu S.Y., Hsueh A.J.W.;
RT "Human stresscopin and stresscopin-related peptide are selective
ligands for the type 2 corticotropin-releasing hormone receptor.";
RL Nat. Med. 7:605-611(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin, and uterus;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Suppress food intake, delays gastric emptying and
decreases heat-induced edema. Might represent an endogenous ligand
for maintaining homeostasis after stress.
CC -!- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
beta.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
FACTOR/UTENSIN I FAMILY OF PEPTIDES.
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CC EMBL: AF320560; AAK52672.1; -
DR EMBL: BC002647; AAH02647.1; ALT_INIT.
DR EMBL: BC022096; AAK22096.1; -
DR MIM: 603902; -
DR InterPro: IPR000187; corticoliberin.
DR SMART: SM00039; CRF; 1.
KW Hormone; Amidation; Signal.
FT SIGNAL 1 19
FT PROPEP 20 70 POTENTIAL.
FT CHAIN 72 112 UROCOCTIN II.
SQ SEQUENCE 112 AA; 12146 MW; 0BFF29A3463723D4 CRC64;
Query Match 100.0%; Score 577; DB 1; Length 112.

Best Local Similarity 100.0%; Pred. No. 4.1e-45;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCALLELLVLMGRVLPVPTPIPTFOLRPONSPTTPRPAASESPSAAPTWPMAAOS 60
DB 1 MTRCALLELLVLMGRVLPVPTPIPTFOLRPONSPTTPRPAASESPSAAPTWPMAAOS 60

QY 61 HCSPTRHPSGRIVSLDVPVIGLQILILEQARARAAREQATTNARILARVGHG 112
DB 61 HCSPTRHPSGRIVSLDVPVIGLQILILEQARARAAREQATTNARILARVGHG 112

RESULT 2

UCN2_RAT STANDARD; PRT; 109 AA.
ID UCN2_RAT
AC Q91WML: 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
GN Urococtin II precursor (Ucn II).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
C SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley; TISSUE=Midbrain;
RA Park J.H., Ju S.K., Lee M.K.;
RT Cloning and analysis of tissue-specific mRNA expression of rat
RT urococtin II";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Suppress food intake, delays gastric emptying and
CC decreases heat-induced edema. Might represent an endogenous ligand
CC for maintaining homeostasis after stress (By similarity).
CC -1- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC beta (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
CC
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CC EMBL: AY044835; AAK98780.1; -
DR InterPro: IPR000187; corticoliberin.
DR SMART: SM00039; CRF; 1.
KW Hormone; Amidation; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 67 POTENTIAL.
FT CHAIN 69 109 UROCOCTIN II.
SQ SEQUENCE 109 AA; AA2B46D8903EDB3E CRC64;

Query Match 54.5%; Score 314.5; DB 1; Length 109;
Best Local Similarity 62.7%; Pred. No. 1e-21;
Matches 69; Conservative 14; Mismatches 24; Indels 3; Gaps 1;

QY 1 MTRCALLELLVLMGRVLPVPTPIPTFOLRPONSPTTPRPAASESPSAAPTWPMAAOS 60
DB 1 MTRCALLELLVLMGRVLPVPTPIPTFOLRPONSPTTPRPAASESPSAAPTWPMAAOS 57

QY 61 HCSPTRHPSGRIVSLDVPVIGLQILILEQARARAAREQATTNARILARVGHG 110
DB 58 NSKASPYLDTRVILSDVPVIGLRLILEQARAKARQAATNQAIIARVGHG 107

RESULT 3
UCN2_MOUSE

ID UCN2_MOUSE STANDARD; PRT; 112 AA.
AC Q99WML: 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
GN Urococtin II precursor (Ucn II).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
C SEQUENCE FROM N.A.
RA STRAIN=BALB/c;
RA MEDLINE=21126973; PubMed=11226328;
RA Reyes T.M., Lewis K., Perrin M.H., Kunitake K.S., Vaughan J.,
RA Aries C.A., Hogenesch J.B., Gulyas J., Rivier J., Vale W.W.,
RA Sawchenko P.E.;
RT "Urococtin II: A member of the corticotropin-releasing factor (CRF)
RT neuropeptide family that is selectively bound by type 2 CRF
RT receptors";
RT Proc. Natl. Acad. Sci. U.S.A. 98:2843-2848(2001).
CC -1- FUNCTION: Suppress food intake, delays gastric emptying and
CC decreases heat-induced edema. Might represent an endogenous ligand
CC for maintaining homeostasis after stress (By similarity).
CC -1- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC beta (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UROTENSIN I FAMILY OF PEPTIDES.

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CC EMBL: AF331517; AAK16157.1; -
DR MGD: MGI:2176375; Ucn2.
DR InterPro: IPR000187; corticoliberin.
DR SMART: SM00039; CRF; 1.
KW Hormone; Amidation; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 70 POTENTIAL.
FT CHAIN 72 112 UROCOCTIN II.
SQ SEQUENCE 112 AA; C87100ZCDA64FB7 CRC64;

Query Match 54.1%; Score 312; DB 1; Length 112;
Best Local Similarity 60.9%; Pred. No. 1.8e-21;
Matches 67; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 1 MTRCALLELLVLMGRVLPVPTPIPTFOLRPONSPTTPRPAASESPSAAPTWPMAAOS 60
DB 1 MTRCALLELLVLMGRVLPVPTPIPTFOLRPONSPTTPRPAASESPSAAPTWPMAAOS 60

QY 61 HCSPTRHPSGRIVSLDVPVIGLQILILEQARARAAREQATTNARILARVGHG 110
DB 61 NSKASPYLDTRVILSDVPVIGLRLILEQARAKARQAATNQAIIARVGHG 110

RESULT 4
UCN3_HUMAN STANDARD; PRT; 161 AA.

AC Q969E3; 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
GN Urococtin III precursor (Ucn III) (Stresscopin).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

RL Nature 378:287-292(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Lewis;
RA Park J.H., Lee Y.J., Kim K.L.;
RT "Detection of rat urocortin in lymphoid tissues: implications for the
functional assessment of urocortin as a novel neuro-immunomodulatory
peptide.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTS IN VITRO TO STIMULATE THE SECRETION OF
ADRENOCORTICOTROPIC HORMONE (ACTH). BINDS WITH HIGH AFFINITY TO
CC CRF RECEPTOR TYPES 1, 2-ALPHA, AND 2-BETA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SAVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
CC -----
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CC -----
DR EMBL: U33935; AAA87566.1; -
DR EMBL: AF093623; AAF63153.1; -
DR InterPro: IPR000187; corticoidberlin.
DR Pfam: PF00473; CRF; 1.
DR SMART: SM00039; CRF; 1.
DR PROSITE: PS00511; CRF; 1.
KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT PROPEP 26 80
FT PEPTIDE 81 120 UROCORTIN.
FT MOD_RES 120 120 AMIDATION (G-121 PROVIDE AMIDE GROUP) (BY
SQ SEQUENCE 122 AA: 13711 MW; 9F0AF834CBFCE7A CRC64;
SIMILARITY).
Query Match 15.4%; Score 89; DB 1; Length 122;
Best Local Similarity 27.5%; Pred. No. 0.15;
Matches 36; Conservative 19; Mismatches 38; Indels 38; Gaps 4;
QY 3 RCALLLVLMIGRLVVPPIPTFQLRPQNSPQTTPRPAAS---ESPS----- 49
DB 6 RALLVALLLV-----QLRPSS-QWSPAAANVYQDPNLKWNPGVRNQ 50
QY 50 -----AAPTPMAAQSICSPTRHSGRIVSLDVPICLLIILEQARARAREQA 99
DB 51 GGGVALLLLAERPRRAGSEPAERQRDDPLSIDLTFTLRLTLELARTOSQRERA 110
QY 100 TTNARILARVG 110
DB 111 EQNRITPDSVG 121
DB 111 EQNRITPDSVG 121
RESULT 7
UCN3_MOUSE
ID UCN3_MOUSE STANDARD; PRT; 164 AA.
AC Q924A4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Urocortin III precursor (ucn III).
GN UCN3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A., SYNTHESIS OF UCN III, AND TISSUE SPECIFICITY.
RA MEDLINE=21310014; PubMed=11416224;
RA Lewis K., Li C., Perrin M.H., Blount A., Knitake K., Donaldson C.,
RA Vaughan J., Reyes T.M., Guljas J., Fischer W., Bilezikjian L.,

RA Rivier J., Sawchenko P.E., Vale W.W.;
RT "Identification of urocortin III, an additional member of the
corticotropin-releasing factor (CRF) family with high affinity for the
RT CRF2 receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7570-7575(2001).
CC -1- FUNCTION: Suppress food intake, delays gastric emptying and
decreases heat-induced edema. Might represent an endogenous ligand
for maintaining homeostasis after stress (By similarity).
CC -1- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
beta.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed in some areas of the brain including
the hypothalamus, amygdala, and brainstem, but is not evident in
the cerebellum, pituitary, or cerebral cortex; it is also
CC expressed peripherally in small intestine and skin.
CC -1- SIMILARITY: BELONGS TO THE SAVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
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CC -----
DR EMBL: AF361944; AAK67318.1; -
DR MGD: MGI:1932970; Ucn3.
KW Hormone; Amidation; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 121
FT CHAIN 123 160
FT MOD_RES 160 160 AMIDATION (G-161 PROVIDE AMIDE GROUP).
SQ SEQUENCE 164 AA: 18063 MW; 93A77CB93DA5E5EC CRC64;
Query Match 15.4%; Score 89; DB 1; Length 164;
Best Local Similarity 36.2%; Pred. No. 0.19;
Matches 17; Conservative 12; Mismatches 18; Indels 0; Gaps 0;
QY 64 PRRHSGRIVSLDVPICLLIILEQARARAREQATTNARILARVG 110
DB 115 PRSDRGTKFTSLDVPNTINMILFNIDKAKNLRKAAANAQMAQIG 161
RESULT 8
UCN1_HUMAN
ID UCN1_HUMAN STANDARD; PRT; 124 AA.
AC P55089;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Urocortin precursor.
GN UCN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96198824; PubMed=8612563;
RA Donaldson C.J., Sutton S.W., Perrin M.H., Corrigan A.Z., Lewis K.A.,
RA Rivier J.E., Vaughan J.M., Vale W.W.;
RT "Cloning and characterization of human urocortin.";
RL Endocrinology 137:2167-2170(1996).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=98292491; PubMed=9628819;
RA Zhao L., Donaldson C.J., Smith G.W., Vale W.W.;
RT "The structures of the mouse and human urocortin genes.";
RL Genomics 50:23-33(1998).
CC -1- FUNCTION: ACTS IN VITRO TO STIMULATE THE SECRETION OF
ADRENOCORTICOTROPIC HORMONE (ACTH). BINDS WITH HIGH AFFINITY TO

CC CRF RECEPTOR TYPES 1, 2-ALPHA, AND 2-BETA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/ORENIN I FAMILY OF PEPTIDES.
CC -----
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CC -----
CC EMBL: AF038633; AAC24204.1; -
CC Genew: HGNC:12516; DCN.
CC MIM: 600945; -
CC InterPro: IPR000187; corticotiberin.
CC Pfam: PF00473; CRF; 1.
CC SMART: SM00039; CRF; 1.
CC PROSITE: PS00511; CRF; 1.
CC Hormone; Amidation; Cleavage on pair of basic residues; signal.
CC SIGNAL 1 25 POTENTIAL.
CC PROPEP 26 82
CC PEPTIDE 83 122 UNICOOTIN.
CC MOD_RES 122 122 AMIDATION (G-123 PROVIDE AMIDE GROUP) (BY
CC SEQUENCE 124 AA; 13458 MW; 4F765DA75DDDA45E CRC64;
CC SIMILARITY).
Query Match 14.0%; Score 81; DB 1; Length 124;
Best Local Similarity 26.7%; Pred. 0.77;
Matches 36; Conservative 15; Mismatches 40; Indels 44; Gaps 5;
QY 3 RCALLLWMLGRVLVPTPIPTFQLRPONSPTTPPAASESPSAAPTPMAOSHC 62
DB 6 RAALLAALLLV-----QLCP-GSSQSPPAAGVQPSL--RMSFGARNG 48
QY 63 S-----PTRHGSRI-----VLSLDPVIGLQILLLEQARRAA 95
DB 49 GGARALLLLAERPPRRAGPRLGLGTAGERPRDNPSTSLDTLFTLTLELTARTQSO 108
QY 96 REQATTNATILARVG 110
DB 109 RERAEONRIIFDSVG 123
RESULT 9
IF35_HUMAN
ID IF35_HUMAN STANDARD: PRT; 357 AA.
AC 000303;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Eukaryotic translation initiation factor 3 subunit 5 (eIF-3 epsilon)
DE (eIF3 p47 subunit).
GN EIF35.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96001678; PubMed=9341143;
RA Asano K., Vornlocher H.-P., Richter Cook N.J., Merrick W.C.,
RA Hinebusch A.G., Hershey J.W.B.;
RT "Structure of cDNAs encoding human eukaryotic initiation factor 3
RT subunits. Possible roles in RNA binding and macromolecular assembly.";
RL J. Biol. Chem. 272:27042-27052(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF
CC METHIONYL-TRNAI AND MRNA ASSOCIATES WITH THE COMPLEX P170-EIF3.
CC SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS.
CC -1- SIMILARITY: BELONGS TO THE PSM7/65.1A FAMILY.
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CC -----
CC EMBL: U94855; AAD03467.1; -
CC EMBL: BC000490; AAH00490.1; -
CC Genew: HGNC:3275; EIF35.
CC MIM: 603914; -
CC InterPro: IPR000555; MOV34.
CC InterPro: IPR003640; MOV34_2.
CC Pfam: PF01398; MOV34; 1.
CC ProDom: PD005425; MOV34_2; 1.
CC SMART: SM00232; JAB.MPN; 1.
CC Initiation factor; Protein biosynthesis.
CC SEQUENCE 357 AA; 37564 MW; 8A70FC6E2BF07737 CRC64;
CC SIMILARITY).
Query Match 14.0%; Score 81; DB 1; Length 357;
Best Local Similarity 26.9%; Pred. 0.21;
Matches 28; Conservative 9; Mismatches 39; Indels 28; Gaps 2;
QY 21 PVTPIPTFQLRPONSPTTPPAASESPSAAPT-----WPMASOSHC 63
DB 12 PATPTVPAAAPASVAPPTAPAAAPVAPAAAPASSSDPAAMATAAPGOTPSAQAQPAQ 71
QY 64 -----PTRHGSRIYSLDPVIGLQILLLEQARRAA 96
DB 72 TPAPALGPALGPFPFGVRLHPVLTASIVSYERRNMGAR 115
RESULT 10
TEGU_EBV
ID TEGU_EBV STANDARD: PRT; 3149 AA.
AC P03186;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Large tegument protein.
GN BPLF1.
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.V., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tuftnell P.S., Barrett B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
CC -1- FUNCTION: TEGUMENT PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
CC EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
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CC -----
CC EMBL: V01555; CAA24839.1; -
CC PIR: A03747; Q0BE8.

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DR InterPro: IPR000585; Hemopexin.
DR InterPro: IPR001818; Matrxin.
DR InterPro: IPR000130; Zn_Mtpeptidse.
DR Pfam: PRF00040; fn2_3.
DR Pfam: PF00045; hemopexin; 4.
DR Pfam: PF00413; Peptidase_M10; 1.
DR PRINTS: PR00013; FNTYPE11.
DR PRINTS: PR00138; MATRXIN.
DR ProDom: PD000995; FN_Type-II; 3.
DR SMART: SM00059; FN2_3.
DR SMART: SM00120; HX; 4.
DR SMART: SM00235; Znmc; 1.
DR PROSITE: PS00023; FIBRONECTIN_2; 3.
DR PROSITE: PS00024; HEMOPEXIN; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
KW Hydroxylase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
KW Collagen degradation; Extracellular matrix; Repeat; Signal.
FT SIGNAL 1 19
FT PROPEP 20 106 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 107 707 92 KDA TYPE IV COLLAGENASE.
FT DOMAIN 223 280 FIBRONECTIN TYPE-II 1.
FT DOMAIN 281 339 FIBRONECTIN TYPE-II 2.
FT DOMAIN 340 397 FIBRONECTIN TYPE-II 3.
FT DOMAIN 513 707 HEMOPEXIN-LIKE.
FT SITE 99 99 CYSTEINE SWITCH (BY SIMILARITY).
FT METAL 401 401 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 402 402 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 405 405 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 411 411 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 516 704 BY SIMILARITY.
FT CONFLICT 76 76 K -> P (IN REF. 2).
FT CONFLICT 100 102 GVP -> ASR (IN REF. 2).
SQ SEQUENCE 707 AA; 78307 MW; 053BCEBDC4D4758F CRC64;

Query Match 13.7% Score 79; DB 1; Length 707;
Best Local Similarity 40.5%; Pred. No. 6.1;
Matches 15; Conservative 4; Mismatches 14; Indels 4; Gaps 1;

Oy 32 PONSPTPTTPRAASESPSAPPTWPAQAOSHCSPTRRP 68
   ||| ||| : ||| ||| : |||
Db 449 PQPATTTTPQPPTAPPTACPTWPTATVTR----PSRHP 481

RESULT 12
MODD_MYCBO
ID MODD_MYCBO STANDARD; PRT; 325 AA.
AC O30620;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Molybdate uptake secreted protein precursor (ALA-PRO rich 45/47 KDA
DE secreted protein) (Immunogenic protein MP132) (Antigen MPT-32) (45-kDa
DE glycoprotein) (Fibronectin attachment protein) (FAP-B).
DE MODD OR APA.
OS Mycobacterium bovis.
OC Bacteria: Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_Taxid=1765;
OX (1)
RN SEQUENCE FROM N.A.
RP STRAIN=BCG;
RC
RA Zhao W., Schorey J.S., Bong-Mastek M., Brown E.J., Ratliff T.L.;
RT "Identification, sequence and characterization of the M. bovis BCG
RT fibronectin attachment protein.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC MODABED FOR MOLVEDBEMUM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE MODD FAMILY.

```

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DR EMBL: AF013569; AAB71842.1;
 KW Molybdenum; Transport; Glycoprotein; Antigen; Signal.
 FT SIGNAL 1 39
 FT CHAIN 1 39
 FT CARBOHYD 49 49
 FT CARBOHYD 57 57
 FT CARBOHYD 66 66
 FT CARBOHYD 316 316
 SQ SEQUENCE 325 AA; 32686 MW; D3419CA3547D91E9 CRC64;

Query Match 13.6%; Score 78.5; DB 1; Length 325;
 Best Local Similarity 28.9%; Pred. No. 3.2;
 Matches 22; Conservative 9; Mismatches 30; Indels 15; Gaps 2;

OY 21 PVTPIPTFQLRPON-----SPQTPPPAASPSAPPTWMAQSHCSPTRRPGSR 71
 Db 43 PAPVPTTAASPPSTAAAPAPAPATPVAPPAAANTPNAQGDPPAAPPADPNAPPPPV 102
 OY 72 IV-----LSLDVPIG 81
 Db 103 IAPNAPQPVRIIDNPGV 118

RESULT 13
 MODD_MYCTU STANDARD; PRT; 325 AA.
 AC Q50906; 008062;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Molybdate uptake secreted protein precursor (Ala-pro rich 45/47 kDa
 DE glycoprotein) (Fibronectin attachment protein) (FAP-B).
 DE MODD OR APA OR RV1860 OR MT1908 OR MTC359.13.
 GN Mycobacterium tuberculosis.
 OS Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RA MEDLINE=96009758; PubMed=7558311;
 RA Laqueyrie A., Miltzer P., Romain F., Eiglmeyer K., Cole S.,
 RA Marchel G.;
 RT "Cloning, sequencing, and expression of the apa gene coding for the
 RT Mycobacterium tuberculosis 45/47-kilodalton secreted antigen
 RT complex";
 RL Infect. Immun. 63:4003-4010(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RA Laqueyrie A.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RA MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekaia F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolony J.F., Nelson W.C., Ormay L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bisai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]

RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RX MEDLINE=9109989; PubMed=1898899;
 RA Nagai S., Wiker H.G., Harboe M., Kinomoto M.;
 RT "Isolation and partial characterization of major protein antigens in
 RT the culture fluid of Mycobacterium tuberculosis.";
 RL Infect. Immun. 59:372-382(1991).
 RN [6]

RP PARTIAL SEQUENCE, AND GLYCOSYLATION.
 RX MEDLINE=95347792; PubMed=7622204;
 RA Dobos K.M., Swiderik K., Khoo K.-H., Brennan P.J., Belisle J.T.;
 RT "Evidence for glycosylation sites on the 45-kilodalton glycoprotein of
 RT Mycobacterium tuberculosis.";
 RL Infect. Immun. 63:2846-2853(1995).
 RN [7]

RP PARTIAL SEQUENCE, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=96196153; PubMed=8626314;
 RA Dobos K.M., Khoo K.-H., Swiderik K.M., Brennan P.J., Belisle J.T.;
 RT "Definition of the full extent of glycosylation of the 45-kilodalton
 RT glycoprotein of Mycobacterium tuberculosis.";
 RL J. Bacteriol. 178:2498-2506(1996).
 CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
 CC MODDED FOR MOLYBDENUM.

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE MODD FAMILY.

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DR EMBL: X80268; CA56555.1;
 DR EMBL: X99258; CA67645.1;
 DR EMBL: 283859; CAB06127.1;
 DR EMBL: AE007048; AAK46179.1;
 DR TIGR: MT1908;
 DR TubercuList; RV1860;
 KW Molybdenum; Transport; Glycoprotein; Antigen; Signal;
 K complete proteome.
 FT SIGNAL 1 39
 FT CHAIN 1 325
 FT CARBOHYD 49 49
 FT CARBOHYD 57 57
 FT CARBOHYD 66 66
 FT CARBOHYD 316 316
 FT CONFLICT 136 136
 SQ SEQUENCE 325 AA; 32720 MW; 59E5D0455A97BED CRC64;

Query Match 13.6%; Score 78.5; DB 1; Length 325;
 Best Local Similarity 28.9%; Pred. No. 3.2;
 Matches 22; Conservative 9; Mismatches 30; Indels 15; Gaps 2;

OY 21 PVTPIPTFQLRPON-----SPQTPPPAASPSAPPTWMAQSHCSPTRRPGSR 71
 Db 43 PAPVPTTAASPPSTAAAPAPAPATPVAPPAAANTPNAQGDPPAAPPADPNAPPPPV 102

RESULT 14	
GCL2_HUMAN	
ID_GCL2_HUMAN	STANDARD; PRT; 837 AA

AC V92630; Q90U4W, 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE General control of amino acid synthesis protein 5-like 2 (EC 2.3.1.-)
 DE (Histone acetyltransferase GCN5) (hSGCN5).
 GN GCN5L2 OR GCN5 OR HGCN5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RN SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RP TISSUE=Liver;
 RC MEDLINE=98278910; PubMed=9611240;
 RA Smith E.R., Belote J.M., Schlitz R.L., Yang X.-J., Moore P.A.,
 RA Berger S.L., Nakatani Y., Allis C.D.;
 RA "Cloning of Drosophila GCN5: conserved features among metazoan GCN5
 RA family members";
 RL Nucleic Acids Res. 26:2948-2954(1998).
 RN [2]
 RN SEQUENCE OF 362-837 FROM N.A. (ISOFORM 1).
 RP TISSUE=Brain;
 RC MEDLINE=96600317; PubMed=8684459;
 RA Yang X.-J., Ostryko V.V., Nishikawa J., Howard B.H., Nakatani Y.;
 RA "A p300/CBP-associated factor that competes with the adenoviral
 RA oncoprotein E1A";
 RL Nature 382:319-324(1996).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
 RP TISSUE=Testis;
 RC MEDLINE=96140426; PubMed=8552087;
 RA Candau R., Moore P.A., Wang L., Barlev N., Ying C.Y., Rosen C.A.,
 RA Berger S.L.;
 RT "Identification of human proteins functionally conserved with the
 RT yeast putative adaptors ADA2 and GCN5";
 RL Mol. Cell. Biol. 16:593-602(1996).
 CC -1- FUNCTION: Functions as a histone acetyltransferase (HAT) to
 CC promote transcriptional activation. Has significant histone
 CC acetyltransferase activity with core histones, but not with
 CC nucleosome core particles.
 CC -1- SUBUNIT: INTERACTS WITH P300, CBP AND ADA2.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1/GCN5-L (SHOWN HERE) AND
 CC 2/GCN5-S; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED, WITH MOST
 CC ABUNDANT EXPRESSION IN OVARY.
 CC -1- SIMILARITY: CONTAINS 1 BROMODOMAIN.
 CC
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 DR EMBL; AF029777; AAC39769.1; -;
 DR EMBL; U57316; AAC50641.1; -;
 DR HSSP; Q92831; 1B91.
 DR TRNSPAC; T01686; -;
 DR Genew; HGNC:4201; GCN5L2.
 DR MIM; 602301; -;
 DR InterPro; IPR0001487; Bromodomain.

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DR   InterPro:IPR000182; GCN5acetyltransf.
DR   Pfam: PF00439; bromodomain; 1.
DR   Pfam: PF00583; Acetyltransf; 1.
DR   PRINTS: PR00503; BROMODOMAIN.
DR   SMART: SM00297; BROMO; 1.
DR   PROSITE: PS00633; BROMODOMAIN_1; FALSE_NEG.
DR   PROSITE: PS50014; BROMODOMAIN_2; 1.
DR   Transcription regulation; Transferase; Nuclear protein;
KW   Alternative splicing.
FT   DOMAIN          555      628      ACETYLTRANSFERASE.
FT   DOMAIN          745      815      BROMODOMAIN.
FT   VARSPLIC        1        410      MISSING (IN ISOFORM 2).
SQ   SEQUENCE      837 AA;  93836 MW;  96D2P67C65627C4C CRC64;
Query Match          13.4%;   Score 77.5;   DB 1;   Length 837;
Best Local Similarity 26.6%;   Pred. No. 9.8;
Matches 29; Conservative 13; Mismatches 36; Indels 31; Gaps 3;

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```

OY      23  TPITFEOLREONSQPTTPPAASESSAAP-----TPMAAQSHCSFTIRPG---- 6
          || || || || || || || || || || || || || || || || || || || || ||
Db      9  TPAPAAQPRLOSPAAPAPITPTPAASAPAPITPTPAAPAPAAAPAGSTGTGPGVGSG 66
OY      70  -----SRIVSLDPVIGLQILILEQARARAREQATNARIARNG 110
          : || || || || || || || || || || || || || || || || || || || ||
Db      69  GAGSGGDPARPGLSQQ-----QRASQKAAQVFGIPRAKKTLEKG 107

```

RESULT 15	
Y091_NPVOP	
ID_Y091_NPVOP	STANDARD:
	PRT: 279 AA

AC 010341; 1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 29.3 kDa protein (ORF92).
 OS *Oryzias pseudotritus* a multicapsid polynucleosis virus (OPNPV).
 CC Viruses: dsDNA viruses, no RNA stage; Baculoviridae;
 CC Nucleopolyhedrovirus.
 OX NCBI_TaxID=164623;
 RN [1]

RT SEQUENCE: 97271300; PubMed:9126251;
 RX MEDLINE:97271300; PubMed:9126251;
 RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
 R0 Rohmann G.F.;
 R1 "The sequence of the *Orygia pseudotsugata* multinnucleocapsid nuclear
 R2 polyhedrosis virus genome.";
 RT Virology 229:381-394(1997).
 CC -1- SIMILARITY: TO CORRESPONDING ORF IN ACMPV.

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CC	-----	
DR	EMBL: U75930; AAC59091.1;	-.
KW	Hypothetical protein.	
SQ	SEQUENCE	279 AA; 29289 MW; 6FA4DAA01009DBF0 CRC64

Query Match	13.2%;	Score 76;	DB 1;	Length 279;
Best Local Similarity	41.3%;	Pred. No. 4.7;		
Matches	19;	Conservative	2;	Mismatches 17;
				Indels 8;
				Gaps 1;

```

QY      23  TPITPOLRPNOSPOTTRPAASESPSAPIPWMAQSCSTTRRP 68
        ||| : : : ||| : : ||| ||| |||
Db      80  TPPTSPTLSPSPSPPTPTSPSPSPPT-----PSPPTSP 117

```

Search completed: March 21, 2003, 11:58:07
Job time : 13.5613 secs

Tue Mar 25 08:25:22 2003

us-09-682-706-2.rspst

Page 1

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 21, 2003, 11:57:47 : Search time 39.7419 Seconds
(without alignments)
580.678 Million cell updates/sec

Title: US-09-682-706-2

Sequence: 1 MTRCALLLMLVLMGRVLVY.....RAAREQATTNARILARVGHG 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	102.5	17.8	151	13	0918E5	0918E5 fugu rubrip
2	95.5	16.6	437	17	082XE3	082XE3 pyrobaculum
3	93.5	16.2	111	5	09VIR3	09VIR3 drosophila
4	87.5	15.2	273	17	082SP1	082SP1 pyrobaculum
5	85.5	14.8	980	16	09RMB5	09RMB5 delnococtus
6	85	14.7	295	12	080MU5	080MU5 comox viru
7	83.5	14.5	155	4	096NM8	096NM8 homo sapien
8	83.5	14.5	955	10	094F92	094F92 chlamydomon
9	83	14.4	267	6	002764	002764 oryctolagus
10	82	14.2	222	16	09ADC6	09ADC6 streptomyce
11	82	14.2	1066	5	09NDO9	09NDO9 dictyosteli
12	82	14.2	1066	5	09NDO9	09NDO9 dictyosteli
13	81.5	14.1	627	17	082ZW0	082ZW0 pyrobaculum
14	81	14.0	774	5	09V620	09V620 drosophila
15	81	14.0	813	5	095TY2	095TY2 drosophila
16	81	14.0	1151	2	08R29	08R29 eubacterium

ALIGNMENTS

17	80.5	14.0	414	17	08TY17	08TY17 methanopyru
18	79.5	13.8	219	16	09RDM5	09RDM5 streptomyce
19	79.5	13.8	363	16	09A2A8	09A2A8 caulobacter
20	79.5	13.8	695	15	08XW4	08XW4 raltosia s
21	79.5	13.8	837	5	09W0A2	09W0A2 drosophila
22	79.5	13.8	3179	12	08V2A4	08V2A4 human herpe
23	79	13.7	119	12	08V107	08V107 herpes simp
24	79	13.7	252	10	094GV3	094GV3 oryza sativ
25	79	13.7	553	16	09RSM4	09RSM4 delnococtus
26	79	13.7	1218	11	09RIM3	09RIM3 rattus norv
27	79	13.7	1241	11	09QYD5	09QYD5 rattus norv
28	79	13.7	1254	11	09RIL1	09RIL1 rattus norv
29	78.5	13.6	198	10	09FRA0	09FRA0 oryza sativ
30	78.5	13.6	286	2	09R640	09R640 mycobacteri
31	78.5	13.6	1751	2	09A0G4	09A0G4 caldicellul
32	78.5	13.6	1937	2	030482	030482 streptomyce
33	78	13.5	287	2	05S144	05S144 aetomonas s
34	78	13.5	499	16	08YLY9	08YLY9 anabaena sp
35	78	13.5	661	11	09JKE3	09JKE3 mus musculi
36	78	13.5	723	11	09JKE4	09JKE4 mus musculi
37	78	13.5	1193	4	094984	094984 homo sapien
38	78	13.5	1641	10	094B60	094B60 oryza sativ
39	77.5	13.4	3536	5	09VZ30	09VZ30 drosophila
40	77.5	13.4	141	4	08TEG2	08TEG2 homo sapien
41	77.5	13.4	259	4	08WV24	08WV24 homo sapien
42	77.5	13.4	400	4	015184	015184 homo sapien
43	77.5	13.4	652	10	094J26	094J26 arabidopsis
44	77.5	13.4	652	10	09LV48	09LV48 arabidopsis
45	77.5	13.4	1691	5	09GRP7	09GRP7 leishmania

RESULT 1

ID	0918E5	PRELIMINARY:	PRT:	151 AA.
AC	0918E5:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Urococtin precursor.			
GN	UCN.			
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Euteleostei;			
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;			
OC	Tetraodontidae; Takifugu.			
OX	NCBI_TaxID=31033;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20485066; PubMed=11032317;			
RA	Brunner B., Gruetznar F., Yaspo M.L., Ropers H.H., Haaf T.,			
RA	Kaischeuer V.M.;			
RT	"Molecular cloning and characterization of the fugu rubripes			
RT	MEST/COG2 imprinting cluster and chromosomal localization in Fugu and			
RT	Tetraodon nigroviridis."			
RL	Chromosome Res. 8:465-476(2000).			
DR	EMBL; AJ251323; CAB96535.1; ..			
KW	SIGNAL.			
FT	SIGNAL.			
SO	SEQUENCE 151 AA; 16686 MW; EBIID52C41A67124 CRC64;			

Query Match 17.8%; Score 102.5; DB 13; Length 151;

Best Local Similarity 24.3%; Pred. No. 0.013;

Matches 36; Conservative 17; Mismatches 48; Indels 47; Gaps 3;

QY	10	MVLMGRVLVYPVPIPIFQRLPQNSPQTP-----RPASESAPVTPMAA- 58
DB	1	MUSLTKTLTLLSVCTPPSSLCILSLDRPLLCDHMAVGLFGDDVDVPGVSPADWASL 60
QY	59	-----QSHCSPTRRHG-----SRIVSLDPIVGL 82

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Bracken C.F., Heston L.L., Edwards R.L., Smith J.L., Bressan R.A.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
RA, Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon *Pyrobaculum aerophilum*.";

Query Match	14.4%	Score 82;	DB 16;	Length 232;
Best Local Similarity	30.9%;	Pred. 0.19;		
Matches	29;	Conservative	10;	Mismatches
			35;	Indels
				Gaps
				4;


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OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY:
RA Stapleton M., Broksstein P., Hong L., Aghayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celisner S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY058444; AAL13673.1; -
DR FlyBase; FBgn0033654; CG8891.
SQ SEQUENCE 813 AA; 88199 MW; 9B9F9571EA08308C CRC64;

Query Match 14.0%; Score 81; DB 5; Length 813;
Best Local Similarity 36.0%; Pred. No. 8.7;
Matches 18; Conservative 8; Mismatches 22; Indels 2; Gaps 1.

QY 21 PVTPIPTFQLRP--QNSPQTTTPPAASESPSAAPTWPMAQSHCSPTRRHP 68
      |:|:|:| | | | | | | | | | | | | | | | | | | | | | | |
Db 482 PLSPWPSWQEAAPQOOQAPQVPPPTQALPRGPATPAIPASYPATPNSNGVPMGHP 531

Search completed: March 21, 2003, 11:59:12
Job time : 43.7419 secs

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OM protein - protein search, using sw model

Run on: March 21, 2003, 11:58:17 ; Search time 19.5097 Seconds
(without alignments)
551.883 Million cell updates/sec

Title: US-09-682-706-2

Sequence: 1 MTRCALLLMVLMIGRLV...RAAREQATTNARILARVGHG 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	89	15.4	122	2	S60262
2	85.5	14.8	980	2	G75523
3	79.5	13.8	363	2	H87702
4	79.5	13.8	3149	1	QOBE8
5	79	13.7	119	2	C40513
6	79	13.7	553	2	C75318
7	79	13.7	707	1	A53796
8	78.5	13.6	325	2	D70666
9	78.5	13.6	1937	2	T03224
10	78	13.5	287	2	S65765
11	78	13.5	476	2	B44997
12	78	13.5	499	2	A12449
13	77.5	13.4	400	2	S58222
14	77	13.3	532	2	I38658
15	76.5	13.3	347	2	H75253
16	76	13.2	270	2	E87649
17	76	13.2	279	2	T10361
18	76	13.2	1113	1	A47106
19	76	13.2	1779	2	T31085
20	75.5	13.1	623	2	A13637
21	75	13.0	837	2	A42112
22	74.5	12.9	133	2	C86473
23	74.5	12.9	315	2	B99607
24	74.5	12.9	421	2	S29599
25	74.5	12.9	527	2	A84645
26	74	12.8	187	1	RHRCE
27	74	12.8	542	2	I39540
28	73.5	12.7	162	2	A45362
29	73.5	12.7	223	2	A87483

30	73	12.7	351	2	S50754	hypothetical prote
31	73	12.7	393	2	T49578	hypothetical prote
32	73	12.7	395	2	B87713	transglucosylase,
33	73	12.7	473	2	S50755	hypothetical prote
34	73	12.7	478	2	T10030	hypothetical prote
35	73	12.7	497	2	F83634	hypothetical prote
36	73	12.7	586	2	H86914	conserved hypothet
37	72.5	12.6	122	2	I46994	corticotropin rele
38	72.5	12.6	163	2	S51109	hypothetical prote
39	72.5	12.6	580	2	T43481	probable mucin DKF
40	72	12.5	303	2	T35616	probable membrane
41	72	12.5	315	2	T06806	proline rich prote
42	72	12.5	474	2	S15921	protein TPX-VT3 -
43	72	12.5	541	2	T48811	hypothetical prote
44	72	12.5	876	2	D70971	hypothetical prote
45	71.5	12.4	387	2	G72506	hypothetical prote

ALIGNMENTS

RESULT 1

S60262

corticotensin - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 05-Nov-1999

C:Accession: S60262
R:Vaughan, J.; Donaldson, C.; Bittencourt, J.; Perrin, M.H.; Lewis, K.; Sutton, Nature 378, 287-292, 1995

A:Title: Urocortin, a mammalian neuropeptide related to fish urotensin I and to A:Reference number: S60262; MUID:96069764; PMID:7477349

A:Accession: S60262
A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-122 <VAV>

A:Cross-references: EMBL:U33935; NID:g1065908; PIDN:AAA87566.1; PID:g1065909
C:Superfamily: diuretic hormone homology <DHH>

F:80-120/Domain: diuretic hormone homology <DHH>

Query Match 15.4%; Score 89; DB 2; Length 122;
Best Local Similarity 27.5%; Pred. No. 0.21;
Matches 36; Conservative 19; Mismatches 38; Indels 38; Gaps 4;

OY 3 RCALLLMVLMIGRLVVPPIPTQLRPONSPOQTPPPAA\$---ESPS----- 49

Db 6 RATLLVALLLLV-----QLRPRESS-QWSPAAANVQDPNLRWNGVRNQ 50

OY 50 -----AAPTPPMAAQSHCSPTRRPGKIVSLDVPITGLDILLEQARARARQDA 99

Db 51 GGGVALLLLLAERPPRRASPPAGERORDDPPLSIDLTFTLLLELANTOSQERRA 110

OY 100 TTNARILARVG 110

Db 111 EQNRIIPDSVG 121

RESULT 2

G75523

probable cell division protein Flk - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: G75523
R:White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: G75523
A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-980 <WHI>
A:Cross-references: GB:AE001900; GB:AE000513; NID:96458079; PIDN:AAF09980.1; PID

A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR0400
 A:Map position: 1

Query Match 14.8%; Score 85.5; DB 2; Length 980;
 Best Local Similarity 36.8%; Pred. No. 3.5;
 Matches 21; Conservative 5; Mismatches 24; Indels 7; Gaps 2;

QY 21 PVTPTPTQLRPNPSP-----OTTPRPAASESPSAATPMPMAQ-SHCSPTRHPS 70
 DB 425 PATPAPAASVPMVPTPRAAARPTRPVSSPGSPFVPSASVSHAAPWDEPAA 481

RESULT 3

hypothetical protein CC3658 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: H87702
 R:Nieman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DebRoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: H87702

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-363 <STO>
 A:Cross-References: GB:AE005673; NID:g13425416; PIDN:AAK25620.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC3658

Query Match 13.8%; Score 79.5; DB 2; Length 363;
 Best Local Similarity 30.9%; Pred. No. 4.7;
 Matches 34; Conservative 13; Mismatches 50; Indels 13; Gaps 4;

QY 5 ALLMLVLMGRVLYVVPVP-----IPTQLRPNPSPQTPPRPAASESPSAATPMPW 56
 DB 30 AIVLSVIVASPVLAQQQPPAMPPLSDYVPTF--GTQSARPAAPTPPGPEAP--VSTAPQ 85
 QY 57 AAGSHCSPTRHPSRIVSLDVPITGLQLLEQARARAARAEQATTNARIL 106
 DB 86 AAPPVGDVTPQAPALDPLA-DLIAQSAQTLDDEAAETAAAPARRRGRIL 134

RESULT 4

QDEB8 BPLFI protein - human herpesvirus 4 (strain B95-8)

C:Species: human herpesvirus 4, Epstein-Barr virus
 C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
 A:Accession: G93065; A03747; S32993
 A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
 A:Reference number: A93065; MUID:85035713; PMID:6092825
 A:Accession: G93065

A:Molecule type: DNA
 A:Residues: 1-3149 <BAN>
 A:Cross-References: EMBL:V01555; NID:g959074; PIDN:CAA24839.1; PID:g1334853
 R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H Nature 310, 207-211, 1984
 A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
 A:Reference number: A03794; MUID:84270667; PMID:6087149
 A:Contents: annotation; protein coding region
 C:Superfamily: human herpesvirus 4 BPLFI protein

Query Match 13.8%; Score 79.5; DB 1; Length 3149;
 Best Local Similarity 26.0%; Pred. No. 40;
 Matches 25; Conservative 14; Mismatches 26; Indels 31; Gaps 5;

QY 18 LVVPVPIPTPTQLR-----PQNSQTPTPRPAASES-----PSAAPTMPW 56

DB 2663 LAAPITLPGPRLMARPFYGAETRASPSDBRSSPPSPKXDSLLPQAPAPQPPSSPW 2722

QY 57 AAOSE-----HCSPTRHPSRIVSLDVPITGL 83
 DB 2723 ASBQGPVYVTLSPHSTPSTASSQKHTIOLP-GLV 2757

RESULT 5

C40513 hypothetical protei ORE3 - human herpesvirus 2

C:Species: human herpesvirus 2
 C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 08-Oct-1999
 C:Accession: C40513
 R:Krause, P.R.; Ostrove, J.M.; Straus, S.E. J. Virol. 65, 5619-5623, 1991
 A:Title: The nucleotide sequence, 5' end, promoter domain, and kinetics of express
 A:Reference number: A40513; MUID:91374627; PMID:1654458
 A:Accession: C40513
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-119 <KRA>
 A:Cross-References: GB:M69065; NID:g330285; PIDN:AAA5852.1; PID:g330288

Query Match 13.7%; Score 79; DB 2; Length 119;
 Best Local Similarity 27.0%; Pred. No. 1.7;
 Matches 31; Conservative 15; Mismatches 29; Indels 40; Gaps 5;

QY 7 LLLMLVLMGRVLYVVPVPTPTQLRPNPSPQTP-----RAASESPSAAP 52
 DB 1 MLVCVAVKGRVRRPPLPP-PLPVSPSPPTSPCPGASAGPGVGCGSPSPVSSP 59

QY 53 TWPW-----AAOSHCS-----PTRHPSRIVSLDVPITGL 86
 DB 60 YSPWAGASPAAGAPCSRDHGMRRPWSAPTRVWMSML---PTGVIORL 110

RESULT 6

C75318 hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: C75318
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, J. M.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: C75318

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-553 <WHI>
 A:Cross-References: GB:AE002044; GB:AE000513; NID:g64559872; PIDN:AAFL1639.1; PID:g
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2090
 A:Map position: 1

Query Match 13.7%; Score 79; DB 2; Length 553;
 Best Local Similarity 29.2%; Pred. No. 7.9;
 Matches 21; Conservative 11; Mismatches 32; Indels 8; Gaps 1;

QY 37 OTTPRPAASESPSAATPMPMAAOSHCSPTRHPSRIVSLDVPITGLQLLEQARARAAR 96
 DB 201 QAAPKPAAPAPQPSDBSLPTTLDBALASDRLP-----DLPEVLLERLMEQEQAAQEQ 252

QY 97 EQATTNARILAR 108
 DB 253 EEPAPAPRAPVR 264

RESULT 7

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Jan-2000
C:Accession: B44997
R:Lew, A.M.; Beck, D.J.
Mol. Biochem. Parasitol. 42, 153-154, 1990
A:Title: The epitope of a protective monoclonal antibody occurs in a region of microheterogeneity of the surface of the parasite
A:Reference number: A44997; PMID:91042831; PMID:1700297
A:Accession: B44997
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-476 <LEW>
A:Cross-references: GB:M34255
C:Superfamily: major merozoite surface antigen
C:Keywords: surface antigen

	Query Match	13.5%	Score 78:	DB 2;	Length 476;	
	Best Local Similarity	28.4%;	Pred. No. 8.4;			
	Matches 25;	Conservative 14;	Mismatches 43;	Indels 6;	Gaps 2;	
Oy	1	MTRCALLIMVLMRLRVIVPVTPIPTFQOLRPONSPOQTTPRPAASESPSAETWPMMAOS	60			
	:	: : : :	:	:	:	
Dd	188	LKRCELDVLVIKAGYIDPEVPAPNPV-APETAPEATAPETAPETAOEAPQPESAIQ	246			
Oy	61	HCSPTRHFGSRIVLSLDPVIGILQLILLE	88			
	:	:	:	:	:	
	247	NNMPMYG-----LYENVDGLONITYTE	269			

RESULT 12
 A12449
 hypothetical protein ali5153 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: A12449
 R:Kaneiko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchihara, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120
 A:Reference number: AB1807, M01D:21595285, PMID:11759840
 A:Accession: A12449
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-499 <KUR>
 A:Cross-References: GB:BA000019; PIDN:BAE76852.1; PID:gl7134291; GSPDB:GM00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: ali5153
 C:Superfamily: Synechocystis hypothetical protein slr1624

	Query Match	13.5%	Score 78;	DB 2;	Length 499;
	Best Local Similarity	34.7%;	Pred. No. 8.8;		
	Matches	17;	Conservative	8;	Mismatches 24; Indels 0; Gaps 0;
	20 VGVVPIPFQRLRPNSSPOTTPRAASESAAFTWMAAQSHCSTTRHP	68			
	: :	:			
D0	392 VTESLDPPEVPVIRPSPTTTPPEQDEVITATSPVTTPPEQPEVNTASD	440			

RESULT 13
 S58222
 PO-rich protein - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
 C:Accession: S58222
 R:Wagner, F.F.; Flegel, W.A.
 submitted to the EMBL Data Library, July 1995
 A:Description: A cDNA, which predicts a protein with PO-rich repeats, isolated from a phage
 A:Reference number: S58222
 A:Accession: S58222
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-400 <MAC>
 A:Cross-references: EMBL:Z50194; NID:g929659; PIDD:CAA90576.1; PID:g929660

[illegible]

RESULT 14
138658
vesicular acetylcholine transporter - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 24-Sep-1999
C:Accession: I38658; I38592
R:Erickson, J.D.; Varouki, H.; Schafer, M.K.; Modi, W.; Diebler, M.; Wehne, J. Biol. Chem. 269, 21929-21932, 1994
A:Title: Functional identification of a vesicular acetylcholine transporter
A:Reference number: I38592; MIMD:94350930; PMID:8071310
A:Accession: I38658
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-532 <RE2>
A:Cross-references: EMBL:U010554; NID:g769847; PIDN:AA932675.1; PID:g769848
A:Accession: I38592
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-532 <RES>
A:Cross-references: EMBL:U09210; NID:g507743; PIDN:AAA20497.1; PID:g507744
C:Genetics:
A:Gene: GDB:SLC18A3; VACHT
A:Cross-references: GDB:386396; OMIM:600336
A:Map position: 10q11.2-10q11.2
C:Superfamily: synaptic vesicle amine transporter

Query Match	13.3%	Score 77	DB 2	Length 533
Best Local Similarity	31.6%	Pred. No. 12		
Matches	30	Conservative 14	Mismatches 29	Indels 22
			Gaps 6	
Oy	4	CALLLLVLMGRVIVVPTPIPTFQLR----	PONSPO----	TPRP-----AASEP 48
	:	: : : :	: :	: :
Db	40	CVALLDLNMLY--MIVIVIPDYIANKMGGEGRPR	TRPEVMEPI	LPPTPANASAYTANT 97
Oy	49	SAAPTWPMAAOSHCSPTRHPCGRIVLSLDVPIGLL	83	
	: :	: :	: :	
Db	98	SASPTAAMPAGSALRP-RIPTE----	SEDKIKGLV	127

RESULT 15
 H75253
 hypothetical protein - *Deinococcus radiodurans* (strain R1)
 C:Species: *Deinococcus radiodurans*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: H75253
 R:White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson,
 M.; Shen, M.; Yamacheyan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R
 A:Reference number: A75250; MUID:20036895; PMID:10567266
 A:Accession: H75253
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-347 <WHI>
 A:Cross-references: GB:AE002089; GB:AE000513; MID:96460427; PIDN:AAF1214.1; PID:g
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2600
 A:Map position: 1

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Page 5

Matches 27; Conservative 9; Mismatches 19; Indels 19; Gaps 5;

QY 6 LLLLMVLMG-----RVLVVPVT-PIPTQLRPQNSPOTTPRPASESPSAPPTPW 56

Db 4 LSLILVALLGCVAPLARAGVQVIFPGPAPA-PVAPAPAPVPVPPPPSA---PAAAPALPV 59

QY 57 A-----AOSHCS 64

Db 60 APAPAPVAOSTCAP 73

Search completed: March 21, 2003, 11:59:48
Job time : 23.5097 secs

1
2



EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 894
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 911
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 636
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 874
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 910
EARLIER	FILING DATE:	1997-08-22
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EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 845
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EARLIER	APPLICATION NUMBER:	60/056, 892
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/057, 761
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/047, 595
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 589
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 588
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 585
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 586
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 590
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 594
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 589
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/047, 589
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/043, 578
EARLIER	FILING DATE:	1997-04-11
EARLIER	APPLICATION NUMBER:	60/043, 576
EARLIER	FILING DATE:	1997-04-11
EARLIER	APPLICATION NUMBER:	60/047, 501
EARLIER	FILING DATE:	1997-05-23
EARLIER	APPLICATION NUMBER:	60/043, 670
EARLIER	FILING DATE:	1997-04-11
EARLIER	APPLICATION NUMBER:	60/056, 632
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 664
EARLIER	FILING DATE:	1997-08-22
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EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 881
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 909
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 875
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 862
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 887
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/056, 908
EARLIER	FILING DATE:	1997-08-22
EARLIER	APPLICATION NUMBER:	60/048, 964
EARLIER	FILING DATE:	1997-06-06
EARLIER	APPLICATION NUMBER:	60/057, 650
EARLIER	FILING DATE:	1997-09-05
EARLIER	APPLICATION NUMBER:	60/056, 884
EARLIER	FILING DATE:	1997-08-22

Page 5

10 RESULT
 1 US-08-641-356-2
 2 Sequence 2, Application US/08641356
 3 Patent No. 5866130
 4 GENERAL INFORMATION:
 5 APPLICANT:
 6 TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
 7 TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCI
 8 TITLE OF INVENTION: AND FOR THE DETECTION OF TUBERCULOSIS
 9 NUMBER OF SEQUENCES: 3
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
 12 ADDRESSEE: NEUSTADT, P.C.
 13 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 14 CITY: Arlington
 15 STATE: Virginia
 16 COUNTRY: U.S.A.
 17 ZIP: 22202
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: Floppy disk
 20 COMPUTER: IBM PC compatible
 21 OPERATING SYSTEM: PC-DOS/MS-DOS
 22 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 23 CURRENT APPLICATION DATA:
 24 APPLICATION NUMBER: US/08/641,356
 25 FILING DATE:
 26 CLASSIFICATION: 536

RESULT 14

US-09-599-366-2
; Sequence 2, Application US/09599366
; Patent No. 6335181
; GENERAL INFORMATION:
; APPLICANT: LAOUEYERIE, Anne
; APPLICANT: MARCHEL, Gilles
; APPLICANT: PESCHER, Pascale
; APPLICANT: ROMAIN, Felix
; TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
; TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF
; FILE REFERENCE: 0660-0138-0DIY
; CURRENT APPLICATION NUMBER: US/09/599,366
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 09/132,528
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 08/641,356
; PRIOR FILING DATE: 1996-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-599-366-2

Query Match

Best Local Similarity 13.6%; Score 78.5; DB 4; Length 325;
Matches 22; Conservative 9; Mismatches 30; Indels 15; Gaps 2;

QY 21 PVTPIPTFOLRPON-----SPQTPRPASESPSAAPTWPMAQSHCSPTRHGSR 71

Db 43 PAPPVPTTAASPSTAAAPPAATVAPPPAAANTPNAGDPNAAAPPADPNAPPPV 102

QY 72 IV-----LSLDVPIG 81

Db 103 IAPNAPQPVRIIDNPVG 118

RESULT 15

US-09-599-366-3
; Sequence 3, Application US/09599366
; Patent No. 6335181

; GENERAL INFORMATION:

; APPLICANT: LAOUEYERIE, Anne
; APPLICANT: MARCHEL, Gilles
; APPLICANT: PESCHER, Pascale
; APPLICANT: ROMAIN, Felix
; TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
; TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF
; FILE REFERENCE: 0660-0138-0DIY
; CURRENT APPLICATION NUMBER: US/09/599,366
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 09/132,528
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 08/641,356
; PRIOR FILING DATE: 1996-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-599-366-3

Query Match

Best Local Similarity 13.6%; Score 78.5; DB 4; Length 325;
Matches 22; Conservative 9; Mismatches 30; Indels 15; Gaps 2;

QY 21 PVTPIPTFOLRPON-----SPQTPRPASESPSAAPTWPMAQSHCSPTRHGSR 71

Db 43 PAPPVPTTAASPSTAAAPPAATVAPPPAAANTPNAGDPNAAAPPADPNAPPPV 102

QY 72 IV-----LSLDVPIG 81

Db 103 IAPNAPQPVRIIDNPVG 118

Search completed: March 21, 2003, 12:00:19
Job time : 20.0645 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 21, 2003, 11:57:47 ; Search time 15.2581 Seconds

(Without alignments)
580.678 Million cell updates/sec

Title: US-09-682-706-3

Perfect score: 200

Sequence: 1 HPGSRIVSLDVLGLLOITL.....ARARAREQATTNARIARV 43

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTIST:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	42.5	151	13	Q918E5
2	63	31.5	42	6	077577
3	60	30.0	162	13	Q8U0H6
4	59	29.5	167	13	Q919D0
5	56.5	28.2	69	6	077778
6	56.5	28.2	559	16	Q8VJH1
7	56	28.0	1203	16	Q9A2I9
8	55	27.5	923	16	Q9PEC5
9	55	27.5	1617	5	Q95YX4
10	53.5	26.8	68	16	Q9S279
11	53.5	26.8	258	2	Q93037
12	53	26.5	79	5	Q20071
13	53	26.5	190	6	Q95M16
14	53	26.5	193	17	Q8T2I8
15	53	26.5	232	5	Q9VPI3
16	53	26.5	257	2	Q53096

17	53	26.5	1420	12	Q9YNB1	Q9YNB1 sugarcane s
18	52.5	26.2	633	17	Q59176	Q59176 pyrococcus
19	52	26.0	224	16	Q8XRB4	Q8XRB4 raietonia s
20	52	26.0	321	16	Q8Y039	Q8Y039 raietonia s
21	52	26.0	375	17	Q9Y949	Q9Y949 aetopyrum p
22	52	26.0	637	5	Q9NGM1	Q9NGM1 giardia lam
23	52	26.0	690	5	Q95XRA	Q95XRA caenorhabd1
24	52	26.0	854	16	Q8YUX0	Q8YUX0 anabaena sp
25	52	26.0	877	16	Q91363	Q91363 pseudomonas
26	51.5	25.8	80	11	Q63816	Q63816 cavia sp. s
27	51.5	25.8	80	11	Q63814	Q63814 mus musculu
28	51.5	25.8	88	6	Q9XSNS	Q9XSNS tupala glis
29	51.5	25.8	632	17	Q8U1H0	Q8U1H0 pyrococcus
30	51.5	25.8	668	16	Q83538	Q83538 treponema p
31	51	25.5	357	16	Q98MX8	Q98MX8 rhizobium l
32	51	25.5	417	16	Q98L77	Q98L77 rhizobium l
33	51	25.5	743	16	Q92T56	Q92T56 rhizobium m
34	51	25.5	1591	11	Q921N9	Q921N9 mus musculu
35	50.5	25.2	104	2	Q87044	Q87044 vibrio chol
36	50.5	25.2	216	16	Q56671	Q56671 vibrio chol
37	50.5	25.2	296	5	Q95ZB8	Q95ZB8 leishmania
38	50.5	25.2	474	4	Q8TEN6	Q8TEN6 homo sapien
39	50.5	25.2	526	16	Q9HXH7	Q9HXH7 pseudomonas
40	50.5	25.2	729	10	Q9C7R6	Q9C7R6 arabidopsis
41	50.5	25.2	729	10	Q8VZK7	Q8VZK7 arabidopsis
42	50.5	25.2	755	11	Q62825	Q62825 rattus norv
43	50	25.0	98	2	Q8VML3	Q8VML3 pseudomonas
44	50	25.0	136	16	Q9KT05	Q9KT05 vibrio chol
45	50	25.0	147	17	Q9HPF8	Q9HPF8 halobacteri

ALIGNMENTS

RESULT 1

Q918E5 PRELIMINARY: PRT: 151 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Uncoarctin precursor.
GN UCN.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=20485066; PubMed=11032317;

RA Brunner B., Gruetznr F., Yaspo M.L., Ropers H.H., Haaf T.,
Kalschauer V.M.; "Molecular cloning and characterization of the Fugu rubripes
RT MEST/COG2 imprinting cluster and chromosomal localization in Fugu and
RT Tetraodon nigroviridis";

RL Chromosome Res. 8:465-476(2000).

DR EMBL; AJ251323; CAB96535.1; -.
KW Signal.

FT SIGNAL.
SQ SEQUENCE 151 AA; 16686 MW; EEB1D52C41A67124 CRC64;

Query Match 42.5%; Score 85; DB 13; Length 151;

Best Local Similarity 42.5%; Pred. No. 0.0011;
Matches 17; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 4 SRIVSLDVLGLLOITLLEQARARAREQATTNARIARV 43

DB 108 SRLTSLDVLPTNIMNVLFDAKAKMLRAKAENARLARI 147

RESULT 2

DR PRINTS: PRO1612; CRFAMILY.
DR SMART: SM00039; CRF: 1.
DR PROSITE: PS00511; CRF: 1.
FT NON_TER 1 69
SQ SEQUENCE 69 AA; 8132 MW; E337469148BC219A CRC64;

Query Match 28.2%; Score 56.5; DB 6; Length 69;
Best Local Similarity 45.5%; Pred. No. 3.3;
Matches 15; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 8 LSLDVLGLQLLEQARARAREQATTNRI 40
DB 37 LSLDVLGLQLLEQARARAREQATTNRI 68

RESULT 6

ID 08YLH1 PRELIMINARY; PRT: 559 AA.
AC 08YLH1:
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Two-component sensor histidine kinase.
GN AL15327.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriuguchi M., Ishikawa K., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL: AP003599; BAB77026.1;
DR InterPro: IPR003594; AtPbind_Atpase.
DR InterPro: IPR004358; Bact_sens_Pt_C.
DR InterPro: IPR003661; His_kinA.
DR InterPro: IPR004359; His_kinA.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000700; PAS-assoc_C.
DR InterPro: IPR000014; PAS-domain.
DR Pfam: PF02518; HATPase_c1.
DR Pfam: PF00785; PAC; 1.
DR Pfam: PF00989; PAS; 1.
DR Pfam: PF00512; signal; 1.
DR PRINTS: PRO0344; BCTRLSENSOR.
DR SMART: SM00387; HATPase_c1.
DR SMART: SM00388; HATPase_c1.
DR SMART: SM00086; PAC; 1.
DR SMART: SM00091; PAS; 1.
DR TIGRFAMs: TIGR00229; sensory_box; 1.
DR PROSITE: PS50109; HIS_KIN; 1.
DR PROSITE: PS50113; PAC; 1.
DR PROSITE: PS50112; PAS; 1.
KW kinase; Complete proteome.
SQ SEQUENCE 559 AA; 62607 MW; 1330C67201155269 CRC64;

Query Match 28.2%; Score 56.5; DB 16; Length 559;
Best Local Similarity 34.8%; Pred. No. 3.1;
Matches 16; Conservative 7; Mismatches 16; Indels 7; Gaps 1;

QY 1 HEGSRVLSUDVLGLQLLE-----QARARAREQATTNARI 39
DB 91 HEGSRVLSUDVLGLQLLE-----QARARAREQATTNARI 136

RESULT 7

Q9A2L9
ID Q9A2L9 PRELIMINARY; PRT: 1203 AA.
AC Q9A2L9:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Helicase, UvrD/Rep family.
GN CC3538.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nieman W.C., Feldblyum T.V., Laub M.R., Ohta N., Maddock J.R.,
RA Eisen J., Heidelberg J.F., Alley M.R., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Hart D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Salzberg S.L., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL: AE006012; AKR25500.1;
DR HSSP: P56255; 1PJR.
DR TIGR: CC3538;
DR InterPro: IPR000212; UvrD-helicase.
DR Pfam: PF00580; UvrD-helicase; 1.
KW Complete proteome.
SQ SEQUENCE 1203 AA; 130264 MW; 497989B5037556A6 CRC64;

Query Match 28.0%; Score 56; DB 16; Length 1203;
Best Local Similarity 48.4%; Pred. No. 83;
Matches 15; Conservative 3; Mismatches 5; Indels 8; Gaps 1;

QY 19 ILLEQARARAREQ-----TTNRIIA 41
DB 365 ILLEQARARAREQ-----TTNRIIA 395

RESULT 8
Q9PEC5
ID Q9PEC5 PRELIMINARY; PRT: 923 AA.
AC Q9PEC5:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE DNA polymerase I.
GN XF1103.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Britones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Coutinho L.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.B., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincini A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garner J., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Lairet F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,

Best Local Similarity 32.6%; Pred. No. 34;
Matches 15; Conservative 8; Mismatches 16; Indels 7; Gaps 1;

OY 2 PGSRVLSLDVILGLDQ-----ILLEQARARAREQATTNARIL 40

Db 132 PREAVEADVILRLQDQWCIPIREIVTEGRSNTRENNAVESARI 177

RESULT 12

Q20071

ID 020071 PRELIMINARY; PRT; 79 AA.

AC Q20071;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

OS Hypothetical 8.7 kDa protein.

GN F35H10.5.

OC Caenorhabditis elegans.

OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Pelodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RX MEDLINE=99069613; PubMed=9851916;

RA None;

RT "Genome sequence of the nematode C. elegans: a platform for

RT investigating biology. The C. elegans Sequencing Consortium.";

RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RT Woessner J.;

RL "The sequence of C. elegans cosmid F35H10.";

RN Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA Waterston R.;

RT "Direct Submission.";

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: U40934; AA81681.1; -

KM Hypothetical protein.

SQ SEQUENCE 79 AA; 8702 MW; F1A115C949ACAE6 CRC64;

Query Match

Best Local Similarity 26.5%; Score 53; DB 5; Length 79;

Matches 11; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

OY 9 SLDVILGLDQILLEQARARAREQATTNAR 38

Db 30 ALAVLTALINLILAQESVARRAQAQANTGSR 59

RESULT 13

Q95M16

ID 095M16 PRELIMINARY; PRT; 190 AA.

AC 095M16;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-JUN-2001 (TREMBLrel. 19, Last sequence update)

DE Corticotrophin-releasing hormone precursor.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RA Buchanan F.C., Thue T.D., Schmutz S.M.;

RT "Sequence analysis of bovine corticotrophin-releasing hormone - a

RT candidate gene for post-natal growth.";

RN Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF340152; AAK83231.1; -
DR InterPro: IPR000187; corticoliberin.
DR InterPro: IPR003620; Urocortin_CRF.
DR Pfam: PF00473; CRF; 1.
DR PRINTS: PR01612; CRFAMILY.
DR ProDom: PD005970; Urocortin_CRF; 1.
DR ProSITE: PS00511; CRF; UNKNOWN_1.

KW Signal.

FT SIGNAL 1 24

FT CHAIN 148 188

SQ SEQUENCE 190 AA; 20737 MW; 9B678054932CD9E CRC64;

Query Match

Best Local Similarity 26.5%; Score 53; DB 6; Length 190;

Matches 12; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

OY 8 ISLDVILGLDQILLEQARARAREQATTNARIL 40

Db 153 ISLDVILGLDQILLEQARARAREQATTNARIL 185

RESULT 14

Q8T218

ID 08T218 PRELIMINARY; PRT; 193 AA.

AC 08T218;

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

GN MK0123.

OC Methanopyrus kandleri.

OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;

OX NCBI_TaxID=2320;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-AV19 / DSM 6324 / JCM 9639;

RX MEDLINE=21927647; PubMed=11930014;

RA Stesarev A.T., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

RA Shcherbina O.V., Shakhova V.V., Belova G.I., Aravind L.,

RA Natale D.A., Rogozin I.B., Yatusov R.L., Wolf Y.I., Stetter K.O.,

RA Malysk A.G., Koonin E.V., Kozlyavkin S.A.;

RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19

RT and monophyly of archaeal methanogens.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

DR EMBL: AE010311; AA01340.1; -

KM Complete proteome.

SQ SEQUENCE 193 AA; 20935 MW; 8BA479B9D31C0612 CRC64;

Query Match

Best Local Similarity 26.5%; Score 53; DB 17; Length 193;

Matches 18; Conservative 6; Mismatches 14; Indels 18; Gaps 2;

OY 2 PGSRVLSLDV-----ILGLQILLEQARARAREQATTNARILA 41

Db 25 PGSGVLVDVDPVPRADRYKDIYRSIVPTTGMYQYRVRTNARAREPA--NKKCLA 78

RESULT 15

Q9VP13

ID 09VP13 PRELIMINARY; PRT; 232 AA.

AC 09VP13;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

Search completed: March 10, 2001

Search completed: March 21, 2003, 11:59:15
Job time : 18.2581 secs

GenCore version 5.1.4_p5_4578
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OK protein - protein search, using sw model

Run on: March 21, 2003, 11:56:43 ; Search time 4.43871 Seconds
(without alignments)
401.802 Million cell updates/sec

Title: US-09-682-706-3

Perfect score: 200
Sequence: 1 HPGSRIVSLDVLGLQLL.....ARARARQATNTNRIARV 43

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	191	95.5	112	1	UCN2_HUMAN
2	138	69.0	109	1	UCN2_RAT
3	133	66.5	112	1	UCN2_MOUSE
4	72	36.0	161	1	UCN3_HUMAN
5	71	35.5	164	1	UCN3_MOUSE
6	63	31.5	122	1	UCN1_MOUSE
7	63	31.5	122	1	UCN1_RAT
8	63	31.5	124	1	UCN1_HUMAN
9	61	30.5	162	1	CRF_XENLA
10	61	30.5	165	1	UR1_ONCOMT
11	61	30.5	187	1	CRF_RAT
12	61	30.5	191	1	CRF_PIG
13	61	30.5	196	1	CRF_HUMAN
14	60	30.0	41	1	UR1_CATCO
15	60	30.0	162	1	CRF1_CATCO
16	60	30.0	162	1	CRF_CARAU
17	59	29.5	145	1	UR1_CARAU
18	59	29.5	145	1	UR1_CYPCA
19	58	29.0	162	1	CRF2_CATCO
20	56.5	28.2	88	1	ARCL_CANFA
21	54	27.0	60	1	UR1_PLAIF
22	54	27.0	190	1	CRF_SHEEP
23	54	27.0	208	1	PIWT_SALTI
24	54	27.0	208	1	PIWT_SALTY
25	53	26.5	232	1	ISPD_DEIRA
26	53	26.5	584	1	SACB_ACEBI
27	52.5	26.2	214	1	YP05_RHOCA
28	51.5	25.8	376	1	5H1D_CAVPO
29	51.5	25.8	572	1	Y062_DEIRA
30	51	25.5	306	1	SDSR_PSES9
31	50.5	25.2	447	1	DIU2_TENMO
32	50	25.0	394	1	PT52_PSEAF
33	49.5	24.8	638	1	LTK2_HUMAN

ALIGNMENTS

34	49	24.5	46	1	DIU2_PERAM
35	49	24.5	122	1	CRF_CANFA
36	49	24.5	139	1	YB02_AERPE
37	49	24.5	462	1	PRTE_ERWCH
38	49	24.5	556	1	YJJK_HAEIN
39	49	24.5	1380	1	CYAA_LEIDO
40	49	24.5	2128	1	SPCB_MOUSE
41	48.5	24.2	340	1	YARC_SCHPO
42	48.5	24.2	482	1	G3B2_HUMAN
43	48.5	24.2	482	1	G3B2_MOUSE
44	48.5	24.2	3674	1	SPCR_HUMAN
45	48	24.0	309	1	PLD_ARCHA

RESULT 1	
UCN2_HUMAN	STANDARD; PRT; 112 AA.
AC	Q96RP3: Q9BUG0:
DT	15-JUN-2002 (rel. 41, Created)
DT	15-JUN-2002 (rel. 41, Last sequence update)
DT	15-JUN-2002 (rel. 41, Last annotation update)
DE	Urocortin II precursor (Ucn II) (Stresscopin-related peptide)
DE	(Urocortin-related peptide).
GN	UCN2 OR SRP OR URP.
OS	Human sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21227098; PubMed=11329063;
RA	Hsu S.Y., Hsueh A.J.W.;
RT	*Human stresscopin and stresscopin-related peptide are selective
RT	ligands for the type 2 corticotropin-releasing hormone receptor.*;
RL	Nat. Med. 7:605-611(2001).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Skin, and Uterus;
RA	Strusberg R.;
RL	Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
CC	- FUNCTION: Suppress food intake, delays gastric emptying and
CC	decreases heat-induced edema. Might represent an endogenous ligand
CC	for maintaining homeostasis after stress.
CC	- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC	beta.
CC	- SUBCELLULAR LOCATION: Secreted.
CC	- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC	FACTOR/ROTENSIN I FAMILY OF PEPTIDES.
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	-----
DR	EMBL; AF320560; AAK52672.1; -
DR	EMBL; BC002647; AAH02647.1; ALT_INIT.
DR	EMBL; BC002096; AAH2096.1; -
DR	MIM: 605902; -
DR	InterPro: IPR00187; corticotiberin.
DR	SMART: SM00039; CRF; 1.
DR	Hormone; Amidation; Signal.
FT	SIGNAL 1 19 POTENTIAL.
FT	PROPEP 72 70 POTENTIAL.
FT	CHAIN 112 AA: 12146 MW; 0EEF29A3463723D4 CRC64;
FT	SEQUENCE

Query Match 95.5%; Score 191; DB 1; Length 112;

```

Best Local Similarity 95.3%; Pred. No. 4.3e-18;
Matches 41; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPGSRIVSLDVPILGLIILEQARARARQATNNARIARV 43
   ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 67 HPGSRIVSLDVPILGLIILEQARARARQATNNARIARV 109

RESULT 2
UCN2_RAT STANDARD; PRT; 109 AA.
ID UCN2_RAT
AC Q91MW1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Urocortin II precursor (Ucn II).
GN UCN2.
OS Rattus norvegicus (Rat).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Midbrain;
RC Park J.H., Ju S.K., Lee M.K.;
"Cloning and analysis of tissue-specific mRNA expression of rat
urocortin II."
RU Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Suppress food intake, delays gastric emptying and
CC decreases heat-induced edema. Might represent an endogenous ligand
CC for maintaining homeostasis after stress (By similarity).
CC -1- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC beta (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
CC -----
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CC -----
DR EMBL; AY04835; AAK98780.1; -
DR InterPro: IPR000187; corticoliberin.
DR SMART: SM00039; CRF; 1.
KW Hormone; Amidation; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 67 POTENTIAL.
FT CHAIN 69 109 UROCORTIN II.
SQ SEQUENCE 109 AA; 11922 MW; AA2B46D8903ED83E CRC64;

Query Match 69.0%; Score 138; DB 1; Length 109;
Best Local Similarity 72.5%; Pred. No. 3.3e-11;
Matches 29; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

OY 4 SRIVSLDVPILGLIILEQARARARQATNNARIARV 43
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 67 TRVLSLDVPILGLIILEQARARARQATNNARIARV 106

RESULT 3
UCN2_MOUSE STANDARD; PRT; 112 AA.
ID UCN2_MOUSE
AC Q99ML8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Urocortin II precursor (Ucn II).
GN UCN2.
OS Mus musculus (Mouse).

OY 4 SRIVSLDVPILGLIILEQARARARQATNNARIARV 43
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 70 TRVLSLDVPILGLIILEQARARARQATNNARIARV 109

RESULT 4
UCN3_HUMAN STANDARD; PRT; 161 AA.
ID UCN3_HUMAN
AC Q969E3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Urocortin III precursor (Ucn III) (Stresscoplin).
GN UCN3 OR SPC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. AND SYNTHESIS OF UCN III.
RA MEDLINE=21310014; Pubmed=11416224;
RA Lewis K., Li C., Perrin M.H., Blount A., Kunitake K., Donaldson C.,
RA Vaughan J., Reyes T.M., Gulyas J., Fischer W., Billezikjian L.,
RA Rivier J., Sawchenko P.E., Vale W.W.;
"Identification of urocortin III, an additional member of the
corticotropin-releasing factor (CRF) family with high affinity for the
CRF2 receptor."
RT Proc. Natl. Acad. Sci. U.S.A. 98:7570-7575(2001).

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RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-21227098; PubMed-11329063;
RA Hsu S.Y., Hsueh A.J.W.;
RT "Human stresscopin and stresscopin-related peptide are selective
RL ligands for the type 2 corticotropin-releasing hormone receptor.";
RL Nat. Med. 7:605-611(2001).
CC -1- FUNCTION: Suppress food intake, delays gastric emptying and
CC decreases heat-induced edema. Might represent an endogenous ligand
CC for maintaining homeostasis after stress.
CC -1- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC beta.
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF361943; AAK67317.1; -.
CC DR EMBL: AY026949; AAK11729.1; -.
CC DR MIM: 605901; -.
CC KW Hormone; Amidation; Signal.
CC FT SIGNAL 1 21 POTENTIAL.
CC FT PROPEP 22 118 UROCORTIN III.
CC FT CHAIN 120 157 AMIDATION (G-158 PROVIDE AMIDE GROUP).
CC FT MOD.RES 157 157
CC SO SEQUENCE 161 AA; 17862 MW; F92B2C8C3087857D CRC64;

Query Match 36.0%; Score 72; DB 1; Length 161;
Best Local Similarity 35.0%; Pred. No. 0.019;
Matches 14; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 4 SRVLSLDVILGLTLLLEQARARAREQATTNARILARY 43
DB 118 TKFTSLDVPNTNIMLFLNIAKAKNLRAQANAANALMAQI 157

RESULT 5
UCN1_MOUSE STANDARD; PRT; 164 AA.
AC Q92A44;
AT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, last sequence update)
DE 15-JUN-2002 (Rel. 41, last annotation update)
DE Urocortin III precursor (Ucn III).
GN UCN3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A., SYNTHESIS OF UCN III, AND TISSUE SPECIFICITY.
RX MEDLINE-21310014; PubMed-11416224;
RA Lewis K., Li C., Perrin M.H., Blount A., Knittake K., Donaldson C.,
RA Vaughan J., Reyes T.M., Gulyas J., Fischer W., Bilezikjian L.,
RA Rivier J., Sawchenko P.E., Vale W.W.;
RT "Identification of urocortin III, an additional member of the
RT corticotropin-releasing factor (CRF) family with high affinity for the
RT CRF2 receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7570-7575(2001).
CC -1- FUNCTION: Suppress food intake, delays gastric emptying and
CC decreases heat-induced edema. Might represent an endogenous ligand
CC for maintaining homeostasis after stress (By similarity).
CC -1- SUBUNIT: Binds with high affinity to CRF receptors 2-alpha and 2-
CC beta.
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- TISSUE SPECIFICITY: Expressed in some areas of the brain including

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CC the hypothalamus, amygdala, and brainstem, but is not evident in
CC the cerebellum, pituitary, or cerebral cortex; it is also
CC expressed peripherally in small intestine and skin.
CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF361944; AAK67318.1; -.
CC DR MGD: MG1:1932970; Ucn3.
CC KW Hormone; Amidation; Signal.
CC FT SIGNAL 1 23 POTENTIAL.
CC FT PROPEP 24 121
CC FT CHAIN 123 160 UROCORTIN III.
CC FT MOD.RES 160 160 AMIDATION (G-161 PROVIDE AMIDE GROUP).
CC SO SEQUENCE 164 AA; 18063 MW; 93A77CB93DA56B5C CRC64;

Query Match 35.5%; Score 71; DB 1; Length 164;
Best Local Similarity 34.1%; Pred. No. 0.026;
Matches 14; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 3 GSRTVSLDVPNTNIMLFLNIAKAKNLRAQANAANALMAQI 43
DB 120 GTRFTSLDVPNTNIMLFLNIAKAKNLRAQANAANALMAQI 160

RESULT 6
UCN1_MOUSE STANDARD; PRT; 122 AA.
AC P81615; O88390;
AT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, last sequence update)
DE 15-JUN-2002 (Rel. 41, last annotation update)
DE Urocortin precursor.
GN UCN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98292491; PubMed-9628819;
RA Zhao L., Donaldson C.J., Smith G.W., Vale W.W.;
RT "The structures of the mouse and human urocortin genes.";
RL Genomics 50:23-33(1998).
CC -1- FUNCTION: ACTS IN VITRO TO STIMULATE THE SECRETION OF
CC ADRENOCORTICOTROPIC HORMONE (ACTH). BINDS WITH HIGH AFFINITY TO
CC CRF RECEPTOR TYPES 1, 2-ALPHA, AND 2-BETA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
CC -----
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CC -----
CC EMBL: AF038632; AAC24202.1; -.
CC MGD: MG1:1276123; Ucn.
CC InterPro: IPR000187; corticoliberin.
CC Pfam: PF00473; CRF; 1.
CC SMART: SM00039; CRF; 1.
CC PROSITE: PS00511; CRF; 1.
CC KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.

```

FT SIGNAL 1 25 POTENTIAL.
 FT PROPEP 26 80 BY SIMILARITY.
 FT PEPTIDE 81 120 UROCORTIN.
 FT MOD_RES 120 120 AMIDATION (G-121 PROVIDE AMIDE GROUP) (BY
 FT SEQUENCE 122 AA; 13557 MW; D2969756F36F5DEA CRC64;

Query Match 31.5%; Score 63; DB 1; Length 122;
 Best Local Similarity 44.4%; Pred. No. 0.22;
 Matches 16; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 8 LSLDYILGLQILLLEQARARAREQATTNARILARY 43
 DB 85 LSLDYILGLQILLLEQARARAREQATTNARILARY 120

RESULT 7
 ID UCN1_RAT STANDARD; PRF; 122 AA.
 AC P55090;

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Urocortin precursor (Corticotensin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96069764; PubMed=7477349;

RA Vaughan J.M., Donaldson C.J., Bittencourt J., Perrin M.H., Lewis K.A.,
 RA Sutton S.W., Chan R., Turbul A., Lovejoy D., Rivier C., Rivier J.E.,
 RA Sarchenko P., Vale W.W.;
 RA "Urocortin, a mammalian neuropeptide related to fish urotensin I and
 RA to corticotropin-releasing factor.";
 RL Nature 378:287-292(1995).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Lewis;
 RA Park J.H., Lee Y.J., Kim K.L.;
 RA "Detection of rat urocortin in lymphoid tissues: implications for the
 RA functional assessment of urocortin as a novel neuro-immunomodulatory
 RA peptide.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: ACTS IN VITRO TO STIMULATE THE SECRETION OF
 CC ABOREOCORTICOTROPIC HORMONE (ACTH). BINDS WITH HIGH AFFINITY TO
 CC CRF RECEPTOR TYPES 1, 2-ALPHA, AND 2-BETA.

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
 CC FACTOR/UROTENSIN I FAMILY OF PEPTIDES.

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CC
 DR EMBL; U33935; AAA87566.1; -;
 DR EMBL; AF093623; AAF63153.1; -;
 DR InterPro: IPR000187; corticoliberin.

DR Pfam: PF00473; CRF; 1.
 DR SMART: SM00039; CRF; 1.
 DR PROSITE: PS00511; CRF; 1.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.

FT SIGNAL 1 25 POTENTIAL.
 FT PROPEP 26 80
 FT PEPTIDE 81 120 UROCORTIN.
 FT MOD_RES 120 120 AMIDATION (G-121 PROVIDE AMIDE GROUP) (BY

FT SEQUENCE 122 AA; 13711 MW; 9F0AF834CBFCE74 CRC64;
 SQ

Query Match 31.5%; Score 63; DB 1; Length 122;
 Best Local Similarity 44.4%; Pred. No. 0.22;
 Matches 16; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 8 LSLDYILGLQILLLEQARARAREQATTNARILARY 43
 DB 85 LSLDYILGLQILLLEQARARAREQATTNARILARY 120

RESULT 8
 ID UCN1_HUMAN STANDARD; PRF; 124 AA.
 AC P55089;

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Urocortin precursor.

OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=96198824; PubMed=8612563;
 RA Donaldson C.J., Sutton S.W., Perrin M.H., Corrigan A.Z., Lewis K.A.,
 RA Rivier J.E., Vaughan J.M., Vale W.W.;
 RA "Cloning and characterization of human urocortin.";
 RL Endocrinology 137:2167-2170(1996).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98292491; PubMed=9628819;
 RA Zhao L., Donaldson C.J., Smith G.W., Vale W.W.;
 RA "The structures of the mouse and human urocortin genes.";
 RL Genomics 50:23-33(1998).
 CC -1- FUNCTION: ACTS IN VITRO TO STIMULATE THE SECRETION OF
 CC ADRENOCORTICOTROPIC HORMONE (ACTH). BINDS WITH HIGH AFFINITY TO
 CC CRF RECEPTOR TYPES 1, 2-ALPHA, AND 2-BETA.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
 CC FACTOR/UROTENSIN I FAMILY OF PEPTIDES.

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CC
 DR EMBL; AF038633; AAC24204.1; -;
 DR Genew; HGNC:12516; UCN.
 DR MIM; 600945; -;
 DR InterPro: IPR000187; corticoliberin.

DR Pfam: PF00473; CRF; 1.
 DR SMART: SM00039; CRF; 1.
 DR PROSITE: PS00511; CRF; 1.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.

FT SIGNAL 1 25 POTENTIAL.
 FT PROPEP 26 82
 FT PEPTIDE 83 122 UROCORTIN.
 FT MOD_RES 122 122 AMIDATION (G-123 PROVIDE AMIDE GROUP) (BY
 FT SEQUENCE 124 AA; 13458 MW; 4F765DA75DD4A5E CRC64;

Query Match 31.5%; Score 63; DB 1; Length 124;
 Best Local Similarity 44.4%; Pred. No. 0.22;
 Matches 16; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 8 LSLDYILGLIQLLEQARARAEQATTNARIARY 43
 DB 87 LSLDTLPHLLRLLLELARIQSOREAREQNRITFDVY 122

RESULT 9

CRE_XENLA
 ID CRE_XENLA STANDARD: PRT: 162 AA.
 AC P49188;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Corticotropin precursor (corticotropin-releasing factor) (CRF)
 DE (Corticotropin releasing hormone).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 CC Xenopodinae; Xenopus.
 CC NCBI_TaxID=8355;
 CC [1]
 CC SEQUENCE FROM N.A.
 RA MEDLINE-93078805; PubMed-1448118;
 RX Stenzel-Poore M.P., Heldwein K.A., Stenzel P., Lee S., Vale W.W.;
 RT "Characterization of the genomic corticotropin-releasing factor (CRF)
 RT gene from Xenopus laevis: two members of the CRF family exist in
 RT amphibians."
 RL Mol. Endocrinol. 6:1716-1724(1992).
 CC -1- FUNCTION: THIS HORMONE FROM HYPOTHALAMUS REGULATES THE RELEASE OF
 CC CORTICOTROPIN FROM PITUITARY GLAND (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SAVAGINE/CORTICOTROPIN-RELEASING
 CC FACTOR/UTROTENSIN I FAMILY OF PEPTIDES.
 CC -----
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 CC -----
 CC EMBL: S50096; AAB24277.1;
 CC InterPro: IPR003620; Urococtin_CRF.
 CC InterPro: IPR000187; corticoliberin.
 CC Pfam: PF00473; CRF; 1.
 CC ProDom: PD005970; Urococtin_CRF; 1.
 CC SMART: SM00039; CRF; 1.
 CC PROSITE: PS00511; CRF; 1.
 CC KW Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues;
 CC Signal.
 CC FT SIGNAL 1 24 POTENTIAL.
 CC FT PROPEP 25 119
 CC FT PEPTIDE 120 160 CORTICOLIBERIN.
 CC FT MOD_RES 160 160 AMIDATION (G-161 PROVIDE AMIDE GROUP).
 CC SQ SEQUENCE 162 AA: 17880 MW: 0265906ACA0636CB CRC64;

Query Match 30.5%; Score 61; DB 1; Length 162;
 Best Local Similarity 39.4%; Pred. No. 0.52;
 Matches 13; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 8 LSLDYILGLIQLLEQARARAEQATTNARIARY 40
 DB 125 LSLDTLPHLLRLLLELARIQSOREAREQNRITFDVY 157

RESULT 10
 URL_ONCMY STANDARD: PRT: 165 AA.
 ID URL_ONCMY
 AC 093448;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Urotensin I precursor.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 CC NCBI_TaxID=8022;
 CC [1]
 CC SEQUENCE FROM N.A.

RA TISSUE-Hypothalamus;
 RX MEDLINE-99348219; PubMed-10417230;
 RA Barsyte D., Tipling D.R., Smart D., Conlon J.M., Baker B.I.,
 RA Lovejoy D.A.;
 RT "Rainbow trout (Oncorhynchus mykiss) urotensin-I: structural
 RT differences between urotensins-I and uroctilins-1;
 RL Gen. Comp. Endocrinol. 115:169-177(1999).
 CC -1- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
 CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CC CORTICOTROPIN-RELEASING FACTOR. THE NONHORMONAL PORTION OF THIS
 CC PRECURSOR MAY BE A UROTENSIN BINDING PROTEIN, UROPHYSIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SAVAGINE/CORTICOTROPIN-RELEASING
 CC FACTOR/UTROTENSIN I FAMILY OF PEPTIDES.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: AJ005264; CA06461.1;
 CC InterPro: IPR003620; Urococtin_CRF.
 CC InterPro: IPR000187; corticoliberin.
 CC Pfam: PF00473; CRF; 1.
 CC ProDom: PD005970; Urococtin_CRF; 1.
 CC SMART: SM00039; CRF; 1.
 CC PROSITE: PS00511; CRF; 1.
 CC KW Hormone; Cleavage on pair of basic residues; Amidation; Signal.
 CC FT SIGNAL 1 18
 CC FT CHAIN 19 120 UROPHYSIN (POTENTIAL).
 CC FT PEPTIDE 123 163 UROTENSIN-I.
 CC FT MOD_RES 163 163 AMIDATION (G-164 PROVIDE AMIDE GROUP) (BY
 CC SIMILARITY).
 CC SQ SEQUENCE 165 AA: 18631 MW: 3263357EEF6E3A1A CRC64;

Query Match 30.5%; Score 61; DB 1; Length 165;
 Best Local Similarity 36.1%; Pred. No. 0.53;
 Matches 13; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 8 LSLDYILGLIQLLEQARARAEQATTNARIARY 43
 DB 128 LSLDTLPHLLRLLLELARIQSOREAREQNRITFDVY 163

RESULT 11
 CRF_RAT
 ID CRF_RAT STANDARD: PRT: 187 AA.
 AC P01143;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Corticoliberin precursor (corticotropin-releasing factor) (CRF)
 DE (Corticotropin releasing hormone).
 GN CRH.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 CC [1]
 CC SEQUENCE FROM N.A.
 RX MEDLINE-86030658; PubMed-3876950;
 RA Jingami H., Mizuno N., Takahashi H., Shibahara S., Furutani Y.,
 RA Imura H., Numa S.;

RT "Cloning and sequence analysis of cDNA for rat
RT corticotropin-releasing factor precursor.",
RL FEBS Lett. 191:63-66(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90331928; PubMed=3274895;
RA Thompson R.C., Seasholtz A.F., Herbert E.;
RT "Rat corticotropin-releasing hormone gene: sequence and
RT tissue-specific expression".
RL Mol. Endocrinol. 1:363-370(1987).
RN [3]
RP SEQUENCE OF 145-185.
RX MEDLINE=83273710; PubMed=6603620;
RA Rivier J., Spiess J., Vale W.;
RT "Characterization of rat hypothalamic corticotropin-releasing
RT factor".
RL Proc. Natl. Acad. Sci. U.S.A. 80:4851-4855(1983).
CC -1- FUNCTION: THIS HORMONE FROM HYPOTHALAMUS REGULATES THE RELEASE OF
CC CORTICOTROPIN FROM PITUITARY GLAND.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UTEROTENSIN I FAMILY OF PEPTIDES.
CC -----
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CC -----
DR EMBL: X03036; CAA26838.1; -;
DR EMBL: M54987; AAA40965.1; -;
DR PIR: A24009; RHRTCE.
DR PIR: A40906; A40906.
DR InterPro: IPR003620; Urocortin_CRF.
DR InterPro: IPR000187; corticoliberin.
DR Pfam: PF00473; CRF; 1.
DR ProDom: PD005970; Urocortin_CRF; 1.
DR SMART: SM00039; CRF; 1.
DR PROSITE: PS00511; CRF; 1.
KW Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues;
KW Signal.
FT SIGNAL 1 24 PROBABLE.
FT PROPEP 25 144
FT PEPTIDE 145 185 CORTICOLIBERIN.
FT MOD_RES 185 185 AMIDATION (G-186 PROVIDE AMIDE GROUP).
SQ SEQUENCE 187 AA; 20680 MW; 911602C82A444CDB CRC64;
Query Match 30.5%; Score 61; DB 1; Length 187;
Best Local Similarity 39.4%; Pred. No. 0.6;
Matches 13; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
Db 8 LSLDYLGLQILLEQARARAREQATTNARIL 40
150 ISLDLTFHLRLREVLAMARAEOALQQAHSNRKLM 182
RESULT 12
ID CRF_PIG STANDARD; PRT; 191 AA.
AC P06296; 062637;
DT 01-JAN-1988 (Rel. 06, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Corticoliberin precursor (Corticotropin-releasing factor) (CRF)
DE (Corticotropin releasing hormone).
GN CRH.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
NCBI_TaxID=9823;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98403942; PubMed=9734873;
RA Mimmack M.L., Parrott R.F., Vellucci S.V.;
RT "Molecular cloning of the porcine corticotropin-releasing factor
RT gene".
RL J. Anim. Sci. 76:2205-2206(1998).
RN [2]
RP SEQUENCE OF 149-189.
RX MEDLINE=86094305; PubMed=3878520;
RA Patchy M., Horvath J., Mason-Garcia M., Szoke B., Schlesinger D.H.,
RA Schally A.V.;
RT "Isolation and amino acid sequence of corticotropin-releasing factor
RT from pig hypothalamus".
RL Proc. Natl. Acad. Sci. U.S.A. 82:8765-8766(1985).
CC -1- FUNCTION: THIS HORMONE FROM HYPOTHALAMUS REGULATES THE RELEASE OF
CC CORTICOTROPIN FROM PITUITARY GLAND.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
CC FACTOR/UTEROTENSIN I FAMILY OF PEPTIDES.
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CC -----
DR EMBL: Y15159; CAA75424.1; -;
DR PIR: A01404; RHPCGE.
DR InterPro: IPR003620; Urocortin_CRF.
DR InterPro: IPR000187; corticoliberin.
DR Pfam: PF00473; CRF; 1.
DR ProDom: PD005970; Urocortin_CRF; 1.
DR SMART: SM00039; CRF; 1.
DR PROSITE: PS00511; CRF; 1.
KW Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues;
KW Signal.
FT SIGNAL 1 24 PROBABLE.
FT PROPEP 25 148
FT PEPTIDE 149 189 CORTICOLIBERIN.
FT MOD_RES 189 189 AMIDATION (G-190 PROVIDE AMIDE GROUP).
FT CONFLICT 188 188 I -> F (IN REF. 2).
SQ SEQUENCE 191 AA; 21042 MW; 166513C1CEDC9B7D CRC64;
Query Match 30.5%; Score 61; DB 1; Length 191;
Best Local Similarity 39.4%; Pred. No. 0.61;
Matches 13; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
Db 8 LSLDYLGLQILLEQARARAREQATTNARIL 40
154 ISLDLTFHLRLREVLAMARAEOALQQAHSNRKLM 186
RESULT 13
ID CRF_HUMAN STANDARD; PRT; 196 AA.
AC P06850;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Corticoliberin precursor (Corticotropin-releasing factor) (CRF)
DE (Corticotropin releasing hormone).
GN CRH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84057755; PubMed=6605851;
RA Shibahara S., Morimoto Y., Furutani Y., Notake M., Takahashi H.,

RA Shimizu S., Horikawa S., Numa S.;
 RT "Isolation and sequence analysis of the human corticotropin-releasing
 factor precursor gene.";
 RL EMBO J. 2:775-779(1983).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89137721; PubMed=2763917;
 RA Robinson B.G., D'Angio L.A. Jr., Pasieka K.B., Majzoub J.A.;
 RT "Preprocorticotropin releasing hormone: cDNA sequence and in vitro
 processing.";
 RL Mol. Cell. Endocrinol. 61:175-180(1989).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP STRUCTURE BY NMR OF 154-194.
 RX MEDLINE=93234434; PubMed=8386360;
 RA Romer C., Bernassau J.-M., Cambillau C., Darbon H.;
 RT "Solution structure of human corticotropin releasing factor by 1H NMR
 and distance geometry with restrained molecular dynamics.";
 RL Protein Eng. 6:149-156(1993).
 CC -1- FUNCTION: THIS HORMONE FROM HYPOTHALAMUS REGULATES THE RELEASE OF
 CC CORTICOTROPIN FROM PITUITARY GLAND.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
 CC FACTOR/UTROENSIN I FAMILY OF PEPTIDES.
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 CC -----
 DR EMBL: V00571; CAA23834.1; -;
 DR EMBL: BC002599; AAH02599.1; -;
 DR EMBL: BC011031; AAH11031.1; -;
 DR PIR: A30327; A30327.
 DR Genew: HGNC:2355; CRH.
 DR MIM: 122560; -;
 DR InterPro: IPR003620; Urocortin_CRF.
 DR InterPro: IPR00187; corticotiberin.
 DR Pfam: PF00473; CRF; 1.
 DR ProDom: PD005970; Urocortin_CRF; 1.
 DR SMART: SM00039; CRF; 1.
 DR PROSITE: PS00511; CRF; 1.
 KW Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues;
 KW Signal.
 FT SIGNAL. 1 24 PROBABLE.
 FT PROPEP 25 153
 FT PEPTIDE 154 194 CORTICOTIBERIN.
 FT MOD_RES 194 194 AMIDATION (G-195 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 196 AA; 21422 MW; 0CCDF05BE364E92 CRC64;
 Query Match 30.5%; Score 61; DB 1; Length 196;
 Best Local Similarity 39.4%; Pred. No. 0.63; 11; Indels 0; Gaps 0;
 Matches 13; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 8 LSLDYLGLQLLEQARARAREQATTNARIL 40
 DB 159 ISLDLFLRLREYLEMARAEQALQAQAHNRKLM 191
 RESULT 14
 ID URL_CANTCO STANDARD; PRT; 41 AA.
 AC P01145;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)

DE Urotensin I.
 OS Catosomus commersoni (White sucker).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Catosomidae; Catosomus.
 CX NCBI_TaxID=7971;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=83016606; PubMed=6981844;
 RA Lederis K., Letter A., McMaster D., Moore G., Schlesinger D.;
 RT "Complete amino acid sequence of urotensin I, a hypotensive and
 RT corticotropin-releasing neuropeptide from Catosomus.";
 RL Science 218:162-164(1982).
 RN (2)
 RP SEQUENCE.
 RX MEDLINE=84025881; PubMed=6313156;
 RA Lederis K., Letter A., McMaster D., Ichikawa T., McCannell K.L.,
 RA Rivier J., Rivier C., Vale W., Fryer J., Kobayashi Y.;
 RT "Isolation, analysis of structure, synthesis, and biological actions
 RT of urotensin I neuropeptides.";
 RL Gen. J. Biochem. Cell Biol. 61:602-614(1983).
 CC -1- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
 CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CC CORTICOTROPIN-RELEASING FACTOR.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
 CC FACTOR/UTROENSIN I FAMILY OF PEPTIDES.
 CC -----
 DR PIR: A01407; UOCCIM.
 DR InterPro: IPR003620; Urocortin_CRF.
 DR InterPro: IPR00187; corticotiberin.
 DR Pfam: PF00473; CRF; 1.
 DR ProDom: PD005970; Urocortin_CRF; 1.
 DR SMART: SM00039; CRF; 1.
 DR PROSITE: PS00511; CRF; 1.
 KW Hormone; Amidation.
 FT MOD_RES 41
 SQ SEQUENCE 41 AA; 4870 MW; AEDB309BFB4A1971 CRC64;
 Query Match 30.0%; Score 60; DB 1; Length 41;
 Best Local Similarity 38.9%; Pred. No. 0.18;
 Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;
 QY 8 LSLDYLGLQLLEQARARAREQATTNARIL 43
 DB 6 ISLDLFLRLREYLEMARAEQALQAQAHNRKLYDEV 41
 RESULT 15
 ID URL_CANTCO STANDARD; PRT; 162 AA.
 AC P13241;
 DT 01-JAN-1990 (rel. 13, Created)
 DT 01-JAN-1990 (rel. 13, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Corticotiberin 1 precursor (corticotropin-releasing factor 1) (CRF 1)
 DE (Corticotropin releasing hormone 1).
 GN CRF1.
 OS Catosomus commersoni (White sucker).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Catosomidae; Catosomus.
 CX NCBI_TaxID=7971;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=89042199; PubMed=3186733;
 RA Okawara Y., Morley S.D., Burzio L.O., Zwiers H., Lederis K.,
 RA Richter D.;
 RT "Cloning and sequence analysis of cDNA for corticotropin-releasing
 RT factor precursor from the teleost fish Catosomus commersoni.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:8439-8443(1988).
 RN (2)
 RP SEQUENCE FROM N.A.

RC TISSUE-Hypothalamus;
 RX MEDLINE=93364569; PubMed=1726976;
 RA Morley S.D., Schonrock C., Richter D., Okawara Y., Lederis K.;
 RT "corticotropin-releasing factor (CRF) gene family in the brain of the
 RT teleost fish *Catostomus commersoni* (white sucker): molecular analysis
 RT predicts distinct precursors for two CRFs and one urotensin I
 RT peptide.";
 RL Mol. Biol. Biotechnol. 1:48-57(1991).
 CC -1- FUNCTION: THIS HORMONE FROM HYPOTHALAMUS REGULATES THE RELEASE OF
 CC CORTICOTROPIN FROM PITUITARY GLAND.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING
 CC FACTOR/UTROTENSIN I FAMILY OF PEPTIDES.
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 CC -----
 DR EMBL: J04116; AAA81529.1; -;
 DR EMBL: S65264; AAA15988.1; -;
 DR PIR: A31343; A31343.
 DR InterPro: IPR003620; Urocortin_CRF.
 DR InterPro: IPR000187; corticoliberin.
 DR Pfam: PF00473; CRF; 1.
 DR PRODOM: PD005970; Urocortin_CRF; 1.
 DR SMART: SM00039; CRF; 1.
 DR PROSITE: PS00511; CRF; 1.
 KW Hormone; Amidation; Hypothalamus; Cleavage on pair of basic residues;
 KW Signal; Multigene family.
 FT SIGNAL 1 24 POTENTIAL.
 FT PROPEP 25 119
 FT PEPTIDE 120 160 CORTICOLIBERIN 1.
 FT MOD RES 160 160 AMIDATION (G-161 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 162 AA; 18508 MW; 4BEBBCBDED291890 CRC64;

Query Match 30.0%; Score 60; DB 1; Length 162;
 Best local similarity 39.4%; Pred. No. 0.7;
 Matches 13; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

OY 8 LSLDYITGLQLLEQARARAREQATINARIL 40
 :||: ||: ||||| :||: ||: ||:
 Db 125 ISLDLTFHLRLREVLAMARAEQLAQAHNRKMM 157

Search completed: March 21, 2003, 11:58:08
 Job time : 5.43871 secs

Db 6 ISLDTFHLREVLRELEMARAEOLAQAHSNRKLM 38

RESULT 3

A45362
C:Superfamily: corticotropin precursor - African clawed frog
N:Alternate names: corticotropin-releasing factor
C:Species: Xenopus laevis (African clawed frog)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
R:Stenzel-Poore, M.P.; Heldwein, K.A.; Stenzel, P.; Lee, S.; Vale, W.W.
Mol. Endocrinol. 6, 1716-1724, 1992
A:Title: Characterization of the genomic corticotropin-releasing factor (CRF) gene from
A:Reference number: A45362; MUID:93078805; PMID:1448118
A:Accession: A45362
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-162 <STE>
A:Cross-references: GB:550096; NID:g260494; PIDN:AAB24277.1; PID:g260495
A:Note: sequence extracted from NCBI backbone (NCBIRP:118818)
C:Genetics:
A:Gene: CRF
C:Superfamily: corticotropin-endorphin; diuretic hormone homology
Keywords: amidated carboxyl end; hormone; hypothalamus
120-160/Domain: diuretic hormone homology <DHH>

Query Match 30.5%; Score 61; DB 2; Length 162;
Best Local Similarity 39.4%; Pred. No. 0.79;
Matches 13; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Oy 8 LSLDYILGLQILLEQARARARARQATTNARIL 40
Db 125 ISLDTFHLREVLRELEMARAEOLAQAHSNRKLM 157

RESULT 4

RHRCF

C:Superfamily: corticotropin-releasing factor; prepro-CRF
N:Alternate names: corticotropin-releasing factor; prepro-CRF
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Nov-1983 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
R:Thompson, R.C.; Seasholtz, A.F.; Herbert, E.
Mol. Endocrinol. 1, 363-370, 1987
A:Title: Rat corticotropin-releasing hormone gene: sequence and tissue-specific expression
A:Reference number: A40906; MUID:90331928; PMID:3274895
A:Accession: A40906
A:Molecule type: DNA
A:Residues: 1-187 <THO>
A:Cross-references: GB:M54987; NID:g203593; PIDN:AAA40965.1; PID:g203594
R:Jingami, H.; Mizuno, N.; Takahashi, H.; Shibahara, S.; Furutani, Y.; Imura, H.; Numa, T.
FEBS Lett. 191, 63-66, 1985
A:Title: Cloning and sequence analysis of cDNA for rat corticotropin-releasing factor prepro-RHRCF
A:Reference number: A91351; MUID:86030658; PMID:3876950
A:Accession: A91351
A:Molecule type: mRNA
A:Residues: 1-187 <JIN>
A:Cross-references: GB:X03036; NID:g56008; PIDN:CAA26838.1; PID:g56009
R:Rivier, J.; Spiess, J.; Vale, W.
Proc. Natl. Acad. Sci. U.S.A. 80, 4851-4855, 1983
A:Title: Characterization of rat hypothalamic corticotropin-releasing factor.
A:Reference number: A93965; MUID:83273710; PMID:6603620
A:Accession: A93965
A:Molecule type: protein
A:Residues: 145-185 <RIY>
C:Comment: Corticotropin from hypothalamus stimulates the release of corticotropin (ACTH) from the anterior pituitary gland, testis, spinal cord, and adrenal gland.
C:Genetics:
A:Gene: CRH
A:Introns: #status absent
A:Note: one intron is in 5' noncoding region

C:Superfamily: corticotropin-endorphin; diuretic hormone homology
C:Keywords: amidated carboxyl end; hormone; hypothalamus
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-187/Product: precorticotropin #status predicted <MAT>
F:145-185/Product: corticotropin #status experimental <CLIN>
F:145-184/Domain: diuretic hormone homology <DHH>
F:165/Modified site: amidated carboxyl end (ILE) (amide in mature form from follow

Query Match 30.5%; Score 61; DB 1; Length 187;
Best Local Similarity 39.4%; Pred. No. 0.91;
Matches 13; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Oy 8 LSLDYILGLQILLEQARARARARQATTNARIL 40
Db 150 ISLDTFHLREVLRELEMARAEOLAQAHSNRKLM 182

RESULT 5

A30327

C:Superfamily: corticotropin precursor - human
N:Alternate names: corticotropin-releasing factor
C:Species: Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
R:Robinson, B.G.; D'Angio Jr., L.A.; Pasieka, K.B.; Majzoub, J.A.
Mol. Cell. Endocrinol. 61, 175-180, 1989
A:Title: Preprocorticotropin releasing hormone: cDNA sequence and in vitro processing
A:Reference number: A30327; MUID:89137721; PMID:2783917
A:Accession: A30327
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-196 <ROB>
R:Sasaki, A.; Tempst, P.; Liotta, A.S.; Margioris, A.N.; Hood, L.E.; Kent, S.B.H.; J. Clin. Endocrinol. Metab. 67, 766-773, 1988
A:Title: Isolation and characterization of a corticotropin-releasing hormone-1-like cDNA
A:Reference number: A60860; MUID:88331316; PMID:3262120
A:Accession: A60860
A:Molecule type: protein
A:Residues: 154-168, X', 170-186 <SNS>
R:Shibahara, S.; Morimoto, Y.; Furutani, Y.; Notake, M.; Takahashi, H.; Shimizu, S.
EMBO J. 2, 775-779, 1983
A:Title: Isolation and sequence analysis of the human corticotropin-releasing factor cDNA
A:Reference number: I38106; MUID:84057755; PMID:6605851
A:Accession: I38106
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-196 <RES>
A:Cross-references: EMBL:V00571; NID:g35355; PIDN:CAA23834.1; PID:g35356
C:Genetics:
A:Gene: GDB:CRH
A:Cross-references: GDB:119804; OMIM:122560
A:Map position: 8q13-8q13
C:Superfamily: corticotropin-endorphin; diuretic hormone homology
C:Keywords: amidated carboxyl end; hormone; hypothalamus; placenta
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-196/Product: precorticotropin #status predicted <MAT>
F:154-194/Product: corticotropin #status predicted <CLIN>
F:154-193/Domain: diuretic hormone homology <DHH>
F:194/Modified site: amidated carboxyl end (ILE) (amide in mature form from follow

Query Match 30.5%; Score 61; DB 2; Length 196;
Best Local Similarity 39.4%; Pred. No. 0.96;
Matches 13; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Oy 8 LSLDYILGLQILLEQARARARARQATTNARIL 40
Db 159 ISLDTFHLREVLRELEMARAEOLAQAHSNRKLM 191

RESULT 6
UOCCIM
wotensin I - white sucker

C:Species: *Catostomus commersoni* (white sucker)

C:Date: 05-Apr-1983 #sequence_revision 05-Apr-1993 #text_change 21-Jan-2000

C:Accession: A94267; A90754; A01407

R:Lederis, K.; Letter, A.; McMaster, D.; Moore, G.; Schlesinger, D.

A:Title: Complete amino acid sequence of urotensin I, a hypotensive and corticotropin-releasing factor

A:Reference number: A94267; PMID:83016606; PMID:6981844

A:Accession: A94267

A:Molecule type: protein

A:Residues: 1-41 <LEI>

R:Lederis, K.; Letter, A.; McMaster, D.; Ichikawa, T.; MacCannell, K.L.; Rivier, J.; Rivier, J.

A:Title: Isolation, analysis of structure, synthesis, and biological actions of urotensin I

A:Reference number: A90754; PMID:84025581; PMID:6313156

A:Accession: A90754

A:Molecule type: protein

A:Residues: 1-41 <LEI>

C:Comment: Urotensin I is found in the teleost caudal neurosecretory system and is involved in the regulation of blood pressure and water balance

C:Superfamily: corticotropin-releasing factor

C:Keywords: amidated carboxyl end; hormone; osmoregulation

F:1-41/Domain: diuretic hormone homology <DHH>

F:41/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 30.0%; Score 60; DB 1; Length 41;

Best Local Similarity 38.9%; Pred. No. 0.26;

Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Db 6 ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

ISLDVILGLLQILFEQARRARAEQATTNARILAV 41

A:Title: Cloning and sequence analysis of cDNA encoding urotensin I precursor.

A:Reference number: A94096; PMID:86094380; PMID:3484550

A:Accession: A94096

A:Molecule type: mRNA

A:Residues: 1-145 <ISH>

A:Cross-references: GB:M1671; NID:9213064; PIDN:AAA9214.1; PID:9213065

A:Experimental source: spinal cord

R:Ichikawa, T.; McMaster, D.; Lederis, K.; Kobayashi, H.

A:Title: Isolation and amino acid sequence of urotensin I, a vasoactive and ACTH-releasing factor

A:Reference number: A93752; PMID:83090718; PMID:6757895

A:Accession: A93752

A:Molecule type: protein

A:Residues: 103-143 <ICH>

C:Comment: Urotensin I is found in the teleost caudal neurosecretory system. It is involved in the regulation of blood pressure and water balance

C:Superfamily: corticotropin-releasing factor

C:Keywords: amidated carboxyl end; hormone; osmoregulation

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-145/Product: urotensin I #status predicted <PRO>

F:103-143/Domain: diuretic hormone homology <DHH>

F:143/Modified site: amidated carboxyl end (Val) (amide in mature form from foli)

Query Match 29.5%; Score 59; DB 1; Length 145;

Best Local Similarity 38.9%; Pred. No. 1.3;

Matches 14; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Db 8 ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

ISLDVILGLLQILFEQARRARAEQATTNARILAV 43

Page 3



RESULT 2
US-08-104-862-8
; Sequence 8, Application US/08104862
; Patent No. 5439885
; GENERAL INFORMATION:
; APPLICANT: Kornreich, Wayne D
; APPLICANT: Hernandez, Jean-Francois
; APPLICANT: Rivier, Jean E F
; APPLICANT: Vale Jr, Wylie W
; TITLE OF INVENTION: CRF Analogs
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 South LaSalle Street, Suite 900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,862
; FILING DATE: 19930810
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/709,091
; FILING DATE: 31-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Schumann, J. J.
; REGISTRATION NUMBER: 20,856
; REFERENCE/DOCKET NUMBER: 54538
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-552-1311
; TELEFAX: 619-552-0095
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-104-862-8
Query Match 32.5%; Score 65; DB 1; Length 41;
Best Local Similarity 41.2%; Pred. No. 0.0099;
Matches 14; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
OY 8 LSLDVLGLQILLLEQARARAREQATTNARILIA 41
|||: ||: ||| |||: ||: ||: |||
6 LSLDLTFHLLREVLLEMARAEQLAQQAHSNRKLMA 39
; RESULT 3
US-08-981-189B-8
; Sequence 8, Application US/08981189B
; Patent No. 6214797
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: UROCORTIN PEPTIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
; STREET: 120 S. LaSalle Street, Suite 1600
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,189B
; FILING DATE: 10-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,144
; FILING DATE: 13-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,223
; FILING DATE: 11-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Schumann, James J.
; REGISTRATION NUMBER: 20,856
; REFERENCE/DOCKET NUMBER: 57611
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-552-1311
; TELEFAX: 858-552-0095
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-981-189B-8
Query Match 31.5%; Score 63; DB 4; Length 40;
Best Local Similarity 44.4%; Pred. No. 0.019;
Matches 16; Conservative 6; Mismatches 14; Indels 0; Gaps 0;
OY 8 LSLDVLGLQILLLEQARARAREQATTNARILARY 43
|||: ||: ||| ||: ||: ||: |||
5 LSLDLTFHLLRLLLELARTQSOREAEQNRILFDSV 40
; RESULT 4
US-09-400-716-10
; Sequence 10, Application US/09400716
; Patent No. 6319900
; GENERAL INFORMATION:
; APPLICANT: Wel, Edward T.
; TITLE OF INVENTION: INHIBITION OF ABNORMAL CELL GROWTH WITH
; FILE REFERENCE: 2900.006US0
; CURRENT FILING DATE: US/09/400,716
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Rat
US-09-400-716-10
Query Match 31.5%; Score 63; DB 4; Length 40;
Best Local Similarity 44.4%; Pred. No. 0.019;
Matches 16; Conservative 6; Mismatches 14; Indels 0; Gaps 0;
OY 8 LSLDVLGLQILLLEQARARAREQATTNARILARY 43
|||: ||: ||| ||: ||: ||: |||
5 LSLDLTFHLLRLLLELARTQSOREAEQNRILFDSV 40
; RESULT 5
US-09-400-716-11
; Sequence 11, Application US/09400716
; Patent No. 6319900
; GENERAL INFORMATION:
; APPLICANT: Wel, Edward T.
; APPLICANT: Slominski, Andrzej T.
; TITLE OF INVENTION: INHIBITION OF ABNORMAL CELL GROWTH WITH

;; TITLE OF INVENTION: CORTICOTROPIN-RELEASING HORMONE ANALOGS
;; FILE REFERENCE: 2900.006050
;; CURRENT APPLICATION NUMBER: US/09/400,716
;; CURRENT FILING DATE: 1999-09-21
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 11
;; LENGTH: 40
;; TYPE: PRT
;; ORGANISM: Human
US-09-400-716-11

Query Match 31.5%; Score 63; DB 4; Length 40;
Best Local Similarity 44.4%; Pred. No. 0.019;
Matches 16; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 8 LSLDVLGLQLLEQARARAREQATNNRILARV 43
DB 5 LSLDLFHLRLTLLRLLELARTQSQRERARQNRIIFDSV 40

RESULT 6
US-08-981-189B-17
; Sequence 17, Application US/08981189B
; Patent No. 6214797
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: UROCORTIN PEPTIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
; STREET: 120 S. LaSalle Street, Suite 1600
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,189B
; FILING DATE: 10-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,144
; FILING DATE: 13-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,223
; FILING DATE: 11-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Schumann, James J.
; REGISTRATION NUMBER: 20,856
; REFERENCE/DOCKET NUMBER: 57611
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-552-1311
; TELEFAX: 858-552-0095
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-981-189B-17

Query Match 31.5%; Score 63; DB 4; Length 41;
Best Local Similarity 44.4%; Pred. No. 0.019;
Matches 16; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 8 LSLDVLGLQLLEQARARAREQATNNRILARV 43
DB 6 LSLDLFHLRLTLLRLLELARTQSQRERARQNRIIFDSV 41

RESULT 7
US-08-981-189B-15
; Sequence 15, Application US/08981189B
; Patent No. 6214797
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: UROCORTIN PEPTIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
; STREET: 120 S. LaSalle Street, Suite 1600
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,189B
; FILING DATE: 10-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,144
; FILING DATE: 13-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,223
; FILING DATE: 11-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Schumann, James J.
; REGISTRATION NUMBER: 20,856
; REFERENCE/DOCKET NUMBER: 57611
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-552-1311
; TELEFAX: 858-552-0095
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-981-189B-15

Query Match 31.5%; Score 63; DB 4; Length 124;
Best Local Similarity 44.4%; Pred. No. 0.074;
Matches 16; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 8 LSLDVLGLQLLEQARARAREQATNNRILARV 43
DB 87 LSLDLFHLRLTLLRLLELARTQSQRERARQNRIIFDSV 122

RESULT 8
US-09-260-846-25
; Sequence 25, Application US/09260846
; Patent No. 6307017
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun Hyuk
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
; FILE REFERENCE: 00537/00900J
; CURRENT APPLICATION NUMBER: US/09/260,846
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 41
; TYPE: PRT
; ORGANISM: mammalian
; FEATURE:

;
;
;
FILING DATE: 199308
CLASSIFICATION: 530

Sequence 2, Application US/08865773
Patent No. 5777073
GENERAL INFORMATION:
APPLICANT: RIVIER, Jean E.F.
TITLE OF INVENTION: CYCLIC CRF ANTAGONIST PEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
STREET: 135 S. LaSalle Street, Suite 900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,773
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/556,578
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,928
FILING DATE: 12-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Schumann, James J.
REGISTRATION NUMBER: 20,856
REFERENCE/DOCKET NUMBER: 57670
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-1311
TELEFAX: 619-552-0095
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-865-773-2

Query Match 30.5%; Score 61; DB 1; Length 41;
Best Local Similarity 39.4%; Pred. No. 0.037;
Matches 13; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 8 LSLDYLGLQILLEQARARAREQATTNARIL 40
:||||: ||: ||| ||| :||: |:::
Db 6 ISLDLTFHLREYLEMARAEQLAQAHNRKLM 38

RESULT 15
US-08-865-773-5
Sequence 5, Application US/08865773
Patent No. 5777073
GENERAL INFORMATION:
APPLICANT: RIVIER, Jean E.F.
TITLE OF INVENTION: CYCLIC CRF ANTAGONIST PEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
STREET: 135 S. LaSalle Street, Suite 900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,773

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/556,578
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,928
FILING DATE: 12-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Schumann, James J.
REGISTRATION NUMBER: 20,856
REFERENCE/DOCKET NUMBER: 57670
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-1311
TELEFAX: 619-552-0095
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-865-773-5

Query Match 30.5%; Score 61; DB 1; Length 41;
Best Local Similarity 39.4%; Pred. No. 0.037;
Matches 13; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 8 LSLDYLGLQILLEQARARAREQATTNARIL 40
:||||: ||: ||| ||| :||: |:::
Db 6 ISLDLTFHLREYLEMARAEQLAQAHNRKLM 38

Search completed: March 21, 2003, 12:00:19
Job time : 6.93548 secs